

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:14:00 ; Search time 7239.48 Seconds  
(without alignments)  
12559.330 Million cell updates/sec

Title: US-09-830-972-1  
Perfect score: 3741  
Sequence: 1 attgctcgtctgggcggcgg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | No. | Score | %<br>Query<br>Match Length | DB   | ID | Description |
|--------|-----|-------|----------------------------|------|----|-------------|
|        | 1   | 772.4 | 20.6                       | 969  | 13 | BU839934    |
|        | 2   | 767.2 | 20.5                       | 785  | 14 | CA511870    |
|        | 3   | 753.4 | 20.1                       | 842  | 13 | BU709149    |
|        | 4   | 745   | 19.9                       | 896  | 14 | CB204418    |
| c      | 5   | 725.6 | 19.4                       | 796  | 14 | CA504729    |
|        | 6   | 709.8 | 19.0                       | 805  | 12 | BI730192    |
|        | 7   | 709.4 | 19.0                       | 822  | 14 | CB521332    |
|        | 8   | 707.8 | 18.9                       | 986  | 13 | BU841009    |
| c      | 9   | 684.6 | 18.3                       | 919  | 13 | BU590898    |
|        | 10  | 673.6 | 18.0                       | 778  | 13 | BU709106    |
|        | 11  | 662.6 | 17.7                       | 777  | 14 | CA320618    |
|        | 12  | 660.4 | 17.7                       | 802  | 14 | CA320635    |
|        | 13  | 659.2 | 17.6                       | 951  | 13 | BQ892001    |
|        | 14  | 648.6 | 17.3                       | 739  | 13 | BU612951    |
|        | 15  | 638.4 | 17.1                       | 742  | 14 | CA320833    |
|        | 16  | 638   | 17.1                       | 638  | 14 | CB576696    |
|        | 17  | 633.8 | 16.9                       | 779  | 14 | CB244702    |
|        | 18  | 633.4 | 16.9                       | 862  | 9  | AU079375    |
|        | 19  | 616   | 16.5                       | 700  | 12 | BI664179    |
|        | 20  | 608.2 | 16.3                       | 935  | 13 | BQ963057    |
|        | 21  | 606.8 | 16.2                       | 751  | 14 | CA315995    |
|        | 22  | 605   | 16.2                       | 673  | 14 | CD349457    |
|        | 23  | 604.8 | 16.2                       | 623  | 14 | CB578453    |
|        | 24  | 604.8 | 16.2                       | 691  | 13 | BU707644    |
|        | 25  | 598   | 16.0                       | 609  | 14 | CB580803    |
|        | 26  | 589.2 | 15.7                       | 914  | 9  | AU079162    |
|        | 27  | 574.2 | 15.3                       | 782  | 12 | BI739239    |
|        | 28  | 570   | 15.2                       | 810  | 10 | BG668013    |
|        | 29  | 568.6 | 15.2                       | 698  | 13 | BU058441    |
|        | 30  | 561   | 15.0                       | 624  | 14 | CB578355    |
|        | 31  | 561   | 15.0                       | 646  | 9  | AA791734    |
|        | 32  | 561   | 15.0                       | 964  | 13 | BQ900768    |
|        | 33  | 560   | 15.0                       | 3533 | 11 | AK034902    |
| c      | 34  | 559.8 | 15.0                       | 567  | 12 | BI289826    |
|        | 35  | 556.8 | 14.9                       | 717  | 14 | BY756291    |
|        | 36  | 556   | 14.9                       | 556  | 14 | CB613337    |
|        | 37  | 550.8 | 14.7                       | 588  | 10 | BF563033    |
|        | 38  | 547.4 | 14.6                       | 691  | 14 | CB525239    |
|        | 39  | 546.8 | 14.6                       | 817  | 14 | CA322433    |
|        | 40  | 545.8 | 14.6                       | 630  | 13 | BQ769602    |
|        | 41  | 543.4 | 14.5                       | 781  | 14 | CA322160    |
| c      | 42  | 542   | 14.5                       | 548  | 10 | BF562389    |
|        | 43  | 541.4 | 14.5                       | 686  | 10 | BB307864    |
|        | 44  | 537.4 | 14.4                       | 679  | 12 | BI149602    |
|        | 45  | 537.4 | 14.4                       | 708  | 12 | BI157842    |

## ALIGNMENTS

## RESULT 1

BU839934

|       |          |        |      |        |                 |
|-------|----------|--------|------|--------|-----------------|
| LOCUS | BU839934 | 969 bp | mRNA | linear | EST 16-OCT-2002 |
|-------|----------|--------|------|--------|-----------------|

DEFINITION AGENCOURT\_8947611 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6329890  
5', mRNA sequence.

ACCESSION BU839934

VERSION BU839934.1 GI:24024317

KEYWORDS EST.

SOURCE      *Mus musculus* (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 969)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL      Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cqapbs-r@mail.nih.gov](mailto:cqapbs-r@mail.nih.gov)

Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.

cDNA Library Preparation: ResGen, Invitrogen Corp

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13783 row: 9 column: 11

High quality sequence stop: 651.

| FEATURES | 5 | 1 | 1 | 1 | 1                   |
|----------|---|---|---|---|---------------------|
|          |   |   |   |   | Location/Qualifiers |

source

1. .969

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/organism="Mus musculus"
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```
/mol type="mRNA"
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```
/db xref="taxon:10090"
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```
/clone="IMAGE:6329890"
```

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/lab host="DH10B (phage-resistant)"
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```
/clone lib="NIH MGC 130"
```

/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;

Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.

Primer: Oligo dT. Average insert size 1.95 kb.

Constructed by ResGen, Invitrogen Corp. Note: this is a

NIH MGC Library."

|      |       |     |   |     |   |     |   |     |   |   |        |
|------|-------|-----|---|-----|---|-----|---|-----|---|---|--------|
| BASE | COUNT | 325 | a | 194 | c | 192 | q | 256 | t | 2 | others |
|------|-------|-----|---|-----|---|-----|---|-----|---|---|--------|

## ORIGIN

Query Match 20.6%; Score 772.4; DB 13; Length 969;

Best Local Similarity 89.6%; Pred. No. 5.8e-112;

Matches 878; Conservative 0; Mismatches 88; Indels 14; Gaps 4;

Qy 2172 CATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTT 2231

Db 1 CATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAATTAAAGAGCCTGAAAGTTT 60

|    |      |  |      |
|----|------|--|------|
| Qy | 2232 | TAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAA  | 2291 |
|    |      |  |      |
| Db | 61   | TAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAA   | 120  |
| Qy | 2292 | AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTCTCTAATTATTCAGAAATAGCAAA    | 2351 |
|    |      |  |      |
| Db | 121  | AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATTCAGAAATAGCAAA   | 180  |
| Qy | 2352 | ATTTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGA | 2411 |
|    |      |  |      |
| Db | 181  | ATTTGAGAAGTCGGTGCTGATCACTGTGAGCTCGTGGATGATTCCCTCACCCGAATCTGA   | 240  |
| Qy | 2412 | ACCAGTTGACTTATTTAGTGTGATGATTCTGAAGTCCCACAAACACAAGAGGAGGC       | 2471 |
|    |      |  |      |
| Db | 241  | ACCAGTTGACTTATTTAGTGTGATGATTCAATTCTGAAGTCCCACAAACACAAGAGGAGGC  | 300  |
| Qy | 2472 | TGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCAGCACAAA--    | 2529 |
|    |      |  |      |
| Db | 301  | TGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAACACAACACAAACA   | 360  |
| Qy | 2530 | -GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCA   | 2588 |
|    |      |  |      |
| Db | 361  | TAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAGGAAAGCCATATTTAGAGTCTTTTCA   | 420  |
| Qy | 2589 | GCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAA   | 2648 |
|    |      |  |      |
| Db | 421  | GCCCAATTTACATATTACAAAAGATGCTGCATCTAATGAAATTCCAACATTGACCAAAAA   | 480  |
| Qy | 2649 | GGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTT   | 2708 |
|    |      |  |      |
| Db | 481  | GGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGATGACTT   | 540  |
| Qy | 2709 | ACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGAT   | 2768 |
|    |      |  |      |
| Db | 541  | ACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTCATCTCCCAT   | 600  |
| Qy | 2769 | TGAGATAATAGATGAATTTCCACGTTTGTGCTAGTCTAAAGATGATTCTCCTAAATTAGC   | 2828 |
|    |      |  |      |
| Db | 601  | TGAGATAATAGATGAGTTTCCACATTTGTGCTAGTCTANAGATGATTCTCCT-----      | 652  |
| Qy | 2829 | CAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGG   | 2888 |
|    |      |  |      |
| Db | 653  | -AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGG   | 711  |
| Qy | 2889 | GGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCC   | 2948 |
|    |      |  |      |
| Db | 712  | NGCCAATTCGTTGCCTTGCTCAGAAATGCCCTGTGACCTTTCTTTCAAGAATACATATCC   | 771  |
| Qy | 2949 | TAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGC   | 3008 |
|    |      |  |      |
| Db | 772  | TAAAGATGAAGCACATGTCTCAGATGAATTCT-CAAAAGTAGGTCCAGTGTATCTAAGGT   | 830  |
| Qy | 3009 | ATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGT   | 3068 |
|    |      |  |      |
| Db | 831  | GCCCCTATTGCTTCCCAATGGTTTCTGCTTGAAATCTCAAATAG-AATGGGCCACATAGT   | 889  |
| Qy | 3069 | TAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGA   | 3128 |



Db 890 TTAACCCAAAGTACTTACGGAAGAAGCAGAGGAAAACTTCCTTCTTGATCCGAGAAAGA 949  
 Qy 3129 GGACAGATCCCTGTCTAGCTG 3148  
 Db 950 GGGACGATCCCTGACAGCTG 969

## RESULT 2

```

CA511870
LOCUS          CA511870              785 bp    mRNA    linear    EST 15-NOV-2002
DEFINITION     UI-R-FJ0-cpx-e-15-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone
                UI-R-FJ0-cpx-e-15-0-UI 5', mRNA sequence.
ACCESSION      CA511870
VERSION        CA511870.1  GI:25002824
KEYWORDS       EST.
SOURCE         Rattus norvegicus (Norway rat)
  ORGANISM     Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE      1  (bases 1 to 785)
  AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE        Normalization and subtraction: two approaches to facilitate gene
                discovery
  JOURNAL      Genome Res. 6 (9), 791-806 (1996)
  MEDLINE      97044477
  PUBMED       8889548
COMMENT        Contact: Soares, MB
                Coordinated Laboratory for Computational Genomics
                University of Iowa
                375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
                Tel: 319 335 8250
                Fax: 319 335 9565
                Email: bento-soares@uiowa.edu
                Tissue Procurement: Dr. James Lin, Universtiy of Iowa
                cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
                cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                Clone Distribution: Researchers may obtain clones from Research
                Genetics (www.resgen.com).
                Seq primer: M13 REVERSE.

```

```

FEATURES             Location/Qualifiers
     source            1. .785
                        /organism="Rattus norvegicus"
                        /mol_type="mRNA"
                        /strain="Sprague-Dawley"
                        /db_xref="taxon:10116"
                        /clone="UI-R-FJ0-cpx-e-15-0-UI"
                        /tissue_type="embryo"
                        /dev_stage="embryo"
                        /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                        /clone_lib="UI-R-FJ0"
                        /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
                        UI-R-FJ0 is a cDNA library containing the following
                        tissue(s): rat embryo. The library was constructed
                        according to Bonaldo, Lennon and Soares, Genome Research,
```



Qy 2299 AAGCTCTCCACTGAGCCAAGTCCAGATTCTCTAATTATTCAGAAATAGCAAAATTCGAG 2358  
 |||  
 Db 601 AAGCTCTCCACTGAGCCAAGTCCAGATTCTCTAATTATTCAGAAATAGCANAATTCGAG 660  
 Qy 2359 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 2418  
 |||  
 Db 661 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 720  
 Qy 2419 GACTTATTTAGTGATGATTCGATTCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATG 2478  
 |||  
 Db 721 GACTTATTTAGTGATGATTCGATTCTGAAGT-CCACANACACAAGAGGAGGCTGTGATG 779  
 Qy 2479 CTCATG 2484  
 |||  
 Db 780 CTCATG 785

# RESULT 3

BU709149

LOCUS BU709149 842 bp mRNA linear EST 26-NOV-2002

DEFINITION UI-M-EW0-caz-o-10-0-UI.r1 NIH\_BMAP\_EW0 Mus musculus cDNA clone  
 IMAGE: 6419553 5', mRNA sequence.

ACCESSION BU709149

VERSION BU709149.1 GI:23642332

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 842)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

## FEATURES

source

Location/Qualifiers

1. .842

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE: 6419553"

/tissue\_type="whole brain"

/dev\_stage="embryo 15.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_EW0"

/note="Organ: brain; Vector: pYX-Asc; Site\_1: EcoR I; Site\_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT      275 a      182 c      181 g      202 t      2 others  
ORIGIN

Query Match                      20.1%;    Score 753.4;    DB 13;    Length 842;  
Best Local Similarity    94.2%;    Pred. No. 5.8e-109;  
Matches 792;    Conservative    0;    Mismatches    48;    Indels      1;    Gaps      1;

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Qy      1677 AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT 1736
          |||
Db      2   AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT 61

Qy      1737 CCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGT 1796
          |||
Db      62   CCTTGTTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGT 121

Qy      1797 GACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGC 1856
          |||
Db      122  GACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGC 181

Qy      1857 ATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGA 1916
          |||
Db      182  ATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGA 241

Qy      1917 CTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCC 1976
          |||
Db      242  CTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTGCCC 301

Qy      1977 ATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTCGCTGATATTGTTATGGAAGC 2036
          |||
Db      302  ATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTTCGCTGATATTGTTATGGAAGC 361

Qy      2037 ACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCC 2096
          |||
Db      362  GCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCC 421

Qy      2097 ACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCC 2156
          |||
Db      422  ACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCC 481

Qy      2157 ACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAA 2216
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Db      482  ACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAATTA 541

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/db\_xref="taxon:10090"  
 /clone="IMAGE:30138586"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_135"  
 /note="Vector: pCMVSPORT6.1; Site\_1: EcoRV; Site\_2: NotI;  
 Normalized full-length enriched library from pooled mouse  
 embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5  
 , and 15.5 (size selected for the 0.5-1 kb fragments)  
 Cloned directionally, priming method: Oligo-dT. cDNA  
 enrichment: >1k bp, Average insert size 1.6k bp.  
 Normalization (Cot value): 7.5 kb. Priming sequence:  
 5'GACTAGTTCTAGATCGCGAGCGGCCGCC(T)3' Tissue contributed by  
 , David Rowe. Library constructed by ResGen, Invitrogen  
 Corp."

BASE COUNT        255 a     177 c     193 g     271 t  
 ORIGIN

Query Match                    19.9%;    Score 745;    DB 14;    Length 896;  
 Best Local Similarity        93.0%;    Pred. No. 1.2e-107;  
 Matches 816;    Conservative        0;    Mismatches    50;    Indels     11;    Gaps        3;

|    |      |  |      |
|----|------|--|------|
| Qy | 2745 | AACATTTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTTCAGTGC  | 2804 |
|    |      |  |      |
| Db | 13   | AACATTTTTCGATTTCATCTCCCATGAGATAATAGATGAGTTTCCACATTTGTTCAGTGC   | 72   |
| Qy | 2805 | TAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAG   | 2864 |
|    |      |  |      |
| Db | 73   | TAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAG       | 123  |
| Qy | 2865 | TGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGA   | 2924 |
|    |      |  |      |
| Db | 124  | TGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGA   | 183  |
| Qy | 2925 | CCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGA   | 2984 |
|    |      |  |      |
| Db | 184  | CCTTTCTTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAA   | 243  |
| Qy | 2985 | AAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACC   | 3044 |
|    |      |  |      |
| Db | 244  | AAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTTGCTTCAAATGTTTCTGCTTTGGAATC   | 303  |
| Qy | 3045 | TCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAA   | 3104 |
|    |      |  |      |
| Db | 304  | TCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAA   | 363  |
| Qy | 3105 | ACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTTCAGCAGAGCT  | 3164 |
|    |      |  |      |
| Db | 364  | ACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTTCAGCAGAGCT  | 423  |
| Qy | 3165 | GAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGT   | 3224 |
|    |      |  |      |
| Db | 424  | GAATAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGT    | 483  |
| Qy | 3225 | GTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAAC | 3284 |
|    |      |  |      |
| Db | 484  | GTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAAC | 543  |

Qy 3285 GGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGT 3344  
 |||  
 Db 544 GGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGT 603

Qy 3345 GATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGA 3404  
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 Db 604 GATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGA 663

Qy 3405 AGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAA 3464  
 |||  
 Db 664 AGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAA 723

Qy 3465 CAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 3524  
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 Db 724 CAGCACAATAAAAGAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 783

Qy 3525 GTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCC-TTGTTCAATGGTCTGACAC 3583  
 | |||  
 Db 784 G-TTGCAGTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTTGTTCAATGGTTTGACAC 842

Qy 3584 TACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCC 3620  
 |||  
 Db 843 TACTGATTTTAGCCCTGATCTCACTCTTCAGTATTCC 879

# RESULT 5

CA504729/c

LOCUS CA504729 796 bp mRNA linear EST 14-NOV-2002

DEFINITION UI-R-FJ0-cpx-e-15-0-UI.s1 UI-R-FJ0 Rattus norvegicus cDNA clone  
 UI-R-FJ0-cpx-e-15-0-UI 3', mRNA sequence.

ACCESSION CA504729

VERSION CA504729.1 GI:24995683

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 796)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. James Lin, Universtiy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

The following repetitive elements were found in this cDNA sequence: 1-35, >POLY\_A#Simple\_repeat (matched compliment)  
Seq primer: M13 FORWARD  
POLYA=Yes.

[illegible]



Qy 1192 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 1251  
 |||  
 Db 493 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 434

Qy 1252 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAA 1311  
 |||  
 Db 433 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAA 374

Qy 1312 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 1371  
 |||  
 Db 373 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 314

Qy 1372 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 1431  
 |||  
 Db 313 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 254

Qy 1432 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTT 1491  
 |||  
 Db 253 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTT 194

Qy 1492 GGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTG 1551  
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 Db 193 GGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTG 134

Qy 1552 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 1611  
 |||  
 Db 133 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 74

Qy 1612 ACAGCAAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 1671  
 |||  
 Db 73 ACAGCAAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 14

Qy 1672 AAAATAGAAGAAA 1684  
 |||  
 Db 13 AAAAAAAAAAAAAA 1

# RESULT 6

BI730192

LOCUS BI730192 805 bp mRNA linear EST 20-SEP-2001

DEFINITION 603349739F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5357385 5', mRNA sequence.

ACCESSION BI730192

VERSION BI730192.1 GI:15707205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 805)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11908 row: n column: 10  
 High quality sequence stop: 802.

FEATURES                      Location/Qualifiers  
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                               /organism="Mus musculus"  
                               /mol\_type="mRNA"  
                               /db\_xref="taxon:10090"  
                               /clone="IMAGE:5357385"  
                               /tissue\_type="retina"  
                               /lab\_host="DH10B (phage-resistant)"  
                               /clone\_lib="NIH\_MGC\_94"  
                               /note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
                               Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
                               Average insert size 3.3 kb. Library enriched for  
                               full-length clones and constructed by Life Technologies.  
                               Note: this is a NIH\_MGC Library."

BASE COUNT            266 a      179 c      165 g      195 t  
 ORIGIN

Query Match                      19.0%;    Score 709.8;    DB 12;    Length 805;  
 Best Local Similarity    93.8%;    Pred. No. 4.4e-102;  
 Matches 751;    Conservative    0;    Mismatches    47;    Indels      3;    Gaps      1;

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Qy      1854 AGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT 1913
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Db      1   AGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT 60

Qy      1914 GGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTG 1973
          |||
Db      61   GGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTG 120

Qy      1974 CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA 2033
          |||
Db      121  CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA 180

Qy      2034 AGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGAGCCAGTGTATC 2093
          |||
Db      181  AGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGAGCCAGTGCATC 240

Qy      2094 CCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCC 2153
          |||
Db      241  CCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCC 300

Qy      2154 CCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAAT 2213
          |||
Db      301  CCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGGAAGAAAT 360

Qy      2214 AAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCAT 2273
          |||
Db      361  TAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCAT 420

Qy      2274 TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA 2333
  
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      ||| |||||
Db      421 TGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAA 480
Qy      2334 TTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGA 2393
      |||||
Db      481 TTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGA 540
Qy      2394 TTCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCC 2453
      |||||
Db      541 TTCCTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCAATTCCTGAAGTCCC 600
Qy      2454 ACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGAC 2513
      |||||
Db      601 ACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGAC 660
Qy      2514 AGTAGCCCGAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCC 2570
      |||||
Db      661 AGTAACACAACACAAACATAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAGGAAAGCC 720
Qy      2571 ATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACAT 2630
      |||||
Db      721 ATATTTAGAGTCTTTTCAGCCCAATTTACATATTACCAAAGATGCTGCATCTACTGAAAT 780
Qy      2631 TCCAACATTGACCAAAAAGGA 2651
      |||||
Db      781 TCCAACATTGACCAAAAAGGA 801

```

# RESULT 7

CB521332

LOCUS CB521332 822 bp mRNA linear EST 28-MAR-2003

DEFINITION UI-M-GH0-cem-h-13-0-UI.r1 NIH\_BMAP\_GH0 Mus musculus cDNA clone

IMAGE: 6841502 5', mRNA sequence.

ACCESSION CB521332

VERSION CB521332.1 GI:29354687

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 822)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES Location/Qualifiers

source 1. .822

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6841502"
/tissue_type="Whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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BASE COUNT      233 a      162 c      181 g      246 t
ORIGIN

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Query Match          19.0%;  Score 709.4;  DB 14;  Length 822;
Best Local Similarity 92.6%;  Pred. No. 5.1e-102;
Matches 771;  Conservative 0;  Mismatches 51;  Indels 11;  Gaps 2;

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Qy      2762 CTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGTCAGTGCTAAAGATGATTCTCCTA 2821
          ||||| |||||||||||||||| ||||||| |||||||||||||||||||||
Db      1 CTCCCATGAGATAATAGATGAGTTTCCACATTTGTGTCAGTGCTAAAGATGATTCTCCT- 59

Qy      2822 AATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCC 2881
          ||||||||||||| ||||||| ||||||| ||||||| |||
Db      60 -----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCC 111

Qy      2882 AAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 2941
          | ||||||| ||| ||||||| ||||||| ||||||| ||||||| |||
Db      112 AGAGCGGGGCCAATTTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 171

Qy      2942 TATATCCTAAAGATGAAGTACATGTTTTAGATGAATTCTCCGAAAATAGGTCCAGTGTAT 3001
          ||||||||||||||| ||||| ||||||| ||||||| ||| |||||||
Db      172 CATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTAT 231

Qy      3002 CTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCA 3061
          ||||| || ||| || ||||||| ||||||| |||| | |||||||
Db      232 CTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCA 291

Qy      3062 GCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAG 3121
          ||||||||| ||||| ||||||| ||||||| ||||||| |||||
Db      292 ACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAG 351

Qy      3122 AGAAAGAGGACAGATCCCTGTCAGCTGTATTGTGTCAGCAGAGCTGAGTAAAACTTCAGTTG 3181
          ||||||||||||||| ||||||| ||||||| ||||||| |||||||

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Db 352 AGAAAGAGGACAGATCCCTGACAGCTGTATTGTGACGAGAGCTGAATAAAACTTCAGTTG 411

Qy 3182 TTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTAT 3241  
 |||

Db 412 TTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTAT 471

Qy 3242 TCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGG 3301  
 |||

Db 472 TCCTGCTGCTGTCTCTGACAGTGTT--TCATTGTGAGTGTAAACGGCCTACATTGCCTTGG 529

Qy 3302 CCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGA 3361  
 |||

Db 530 CCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGA 589

Qy 3362 AATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGG 3421  
 |||

Db 590 AATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCCATATCAGAGG 649

Qy 3422 AATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAGAAG 3481  
 |||

Db 650 AATTGGTTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAGAAT 709

Qy 3482 TGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTGATGT 3541  
 |||

Db 710 TGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCCTGAAGTTTGAGTGTGATGT 769

Qy 3542 GGGTGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTA 3594  
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Db 770 GGGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGACTTTA 822

# RESULT 8

BU841009

LOCUS BU841009 986 bp mRNA linear EST 16-OCT-2002

DEFINITION AGENCOURT 10187690 NIH\_MGC\_134 Mus musculus cDNA clone  
 IMAGE:6518816 5', mRNA sequence.

ACCESSION BU841009

VERSION BU841009.1 GI:24025409

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 986)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14101 row: c column: 09

High quality sequence start: 21  
High quality sequence stop: 644.

FEATURES  
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1. .986  
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/mol\_type="mRNA"  
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/clone="IMAGE:6518816"  
/tissue\_type="undifferentiated limb"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_134"  
/note="Vector: pCMV-SPORT6.1.ccdB; Site\_1: EcoRV; Site\_2:  
NotI; Cloned unidirectionally. Primer: Oligo dT. Average  
insert size 1.7 kb. Constructed by ResGen, Invitrogen  
Corp. Note: this is a NIH\_MGC Library."  
BASE COUNT 302 a 227 c 208 g 248 t 1 others  
ORIGIN

Query Match 18.9%; Score 707.8; DB 13; Length 986;  
Best Local Similarity 87.8%; Pred. No. 8.9e-102;  
Matches 832; Conservative 0; Mismatches 103; Indels 13; Gaps 5;

Qy 1728 AAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTT 1787  
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Db 29 AAATCCTTTCCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTT 88  
  
Qy 1788 ATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGT 1847  
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Db 89 ATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGT 148  
  
Qy 1848 TCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAAC 1907  
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Db 149 TCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAAC 208  
  
Qy 1908 AAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACA 1967  
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Db 209 AAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACA 268  
  
Qy 1968 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGT 2027  
|||||  
Db 269 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGT 328  
  
Qy 2028 TATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAG 2087  
|||||  
Db 329 TATGGAAGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAG 388  
  
Qy 2088 TGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGA 2147  
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Db 389 TGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGA 448  
  
Qy 2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207  
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Db 449 AAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGGA 508  
  
Qy 2208 AGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATAT 2267  
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Db 509 AGAAATTAAAGAGCCTGANAGTTTAAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATAT 568

Qy 2268 ATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTT 2327  
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 Db 569 ATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTT 628

Qy 2328 CTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGT 2387  
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 Db 629 CTCTAATTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGT 688

Qy 2388 GGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGA 2447  
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 Db 689 GGATGATTCCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATCCCTGA 748

Qy 2448 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC 2507  
 |||||  
 Db 749 AGTCCCACCAACACAAGAGGAAGCTGTGATGCTTATGAAAGAGAGTCTCACCTGAATGTC 808

Qy 2508 TGAGACAGTAGCCCAGC----ACAAAGAGGAGAGACTTAGTG----CCTCACCTCAGGAG 2559  
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 Db 809 TGAGACAGTTACCCCAACATAAGGGAGAGACTTAGTGCTTTCCCTCCGGAGGGT 868

Qy 2560 CTAGGAAAGCCATATTTAGAGTCTTTT--CAGCCCAATTTACATAGT--ACAAAAGATGC 2615  
 | |  
 Db 869 AGAAAAGGCCCTATTTTAGAGTCTTTTCAGCCCAATTTACCTATTTACCAAAGGATGC 928

Qy 2616 TGCAT-CTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTT 2662  
 ||| |  
 Db 929 TGCCTCCTAATGAAAATTCCACCTTTGGCCCAAAGGGAGACCATTTT 976

# RESULT 9

BU590898/c

LOCUS BU590898 919 bp mRNA linear EST 20-SEP-2002

DEFINITION AGENCOURT\_8798355 NIH\_MGC\_137 Mus musculus cDNA clone IMAGE:6430691  
 5', mRNA sequence.

ACCESSION BU590898

VERSION BU590898.1 GI:23242434

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 919)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)

cDNA Library Preparation: Catherine Lee, Endocrine Pancreas  
 Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBD8 row: e column: 12

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FEATURES             Location/Qualifiers
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                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:6430691"
                        /lab_host="DH10B"
                        /clone_lib="NIH_MGC_137"
                        /note="Organ: pancreas; Vector: pSPORT1; Site_1: SalI;
                        Site_2: NotI; Library consists of a pool of clones
                        rearranged from the following libraries: Melton normalized
                        mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
                        islets 1 MIS1-A, and Kaestner ngn3 wt. Clones rearranged in
                        the laboratory of K. Kaestner (University of Pennsylvania
                        ). Note: this is a NIH_MGC Library."

BASE COUNT      235 a      208 c      162 g      314 t
ORIGIN

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Query Match 18.3%; Score 684.6; DB 13; Length 919;  
Best Local Similarity 88.5%; Pred. No. 4.1e-98;  
Matches 794; Conservative 0; Mismatches 84; Indels 19; Gaps 4;

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| Qy | 805  | CCTGTGATACCTCTCTCTG--CAGAAAAAATTATGGATTGTGAGCA-GCCAGGTAAC     | 861  |
|    |      |   |      |
| Db | 897  | CCTGTGATACCTCCCTTGACAGAAAAATATTATGGATTTGAAGGAGCACCCCAGGTAAC   | 838  |
| Qy | 862  | ACTGTTTCGTCTGGTC-AAGAGGATTTCCCATCTGTCTCTGCTTGAACTGCTGCCTCTCT  | 920  |
|    |      |   |      |
| Db | 837  | CATGTTTCGTCTCATGTCTAAGAGGATTTCCCATCTGTCTGTATGAACTGTTGCCTCTCT  | 778  |
| Qy | 921  | TCCTTCTCTATCTCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTT  | 980  |
|    |      |   |      |
| Db | 777  | TCCTGGTATATATACTATCCCAACTGTTTCTTTTAAAGAACACGGATTCTTTGGTAACCTT | 718  |
| Qy | 981  | ATCAGCAGTGTCTATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGA  | 1040 |
|    |      |   |      |
| Db | 717  | ATCAGCAGTGGCATCCTCAGAAGGAACATTGAAGTAACCTTTAAATGAAGCTTCTAGAGA  | 658  |
| Qy | 1041 | GTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAAATTTTCAGAATT | 1100 |
|    |      |   |      |
| Db | 657  | ATTCCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGAGTTTTCAGTATT  | 598  |
| Qy | 1101 | AGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATT  | 1160 |
|    |      |   |      |
| Db | 597  | AGAATAGTCAGAAATGGGATCATCTTTCAATGGGTCCCCAAAAGGAGAGTCAGCCATGTT  | 538  |
| Qy | 1161 | AGTAGAAAACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGATTTAGTTTG    | 1220 |
|    |      |   |      |
| Db | 537  | AGTAGAAAAATTAAAGGAAGAAGTAATTGTGAGGAGTAAAGGCAAAGAGGATTTAGTTTG  | 478  |
| Qy | 1221 | TAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGA            | 1265 |
|    |      |   |      |
| Db | 477  | TAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGTCCCTTACTAAAGTGGTTAAAGA  | 418  |
| Qy | 1266 | AGACAGAGTTGTGTCTCCAGAAAAGCAATGGACATTTTAAATGAAATGCAGATGTCAAGT  | 1325 |



|    |      |   |      |
|----|------|---|------|
| Db | 417  | AGTCGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGAAAATGTCAGT  | 358  |
| Qy | 1326 | AGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGT  | 1385 |
| Db | 357  | GGTAGCACCTCTGAGGGAAGAGTATGCAGATTTTAAAGCCATTTGAACAAGCATGGGAAGT | 298  |
| Qy | 1386 | GAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAAAGTAA  | 1445 |
| Db | 297  | GAAAGATACTTATGAGGGAAGTAGGGATGTTCTGGTTGCTAGAGATAATATGGAAAGTAA  | 238  |
| Qy | 1446 | AGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGATAGTGA   | 1505 |
| Db | 237  | AGTGGGCAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAAGTCATGGGAAGGATAGTGA  | 178  |
| Qy | 1506 | AGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGCTCCAG   | 1565 |
| Db | 177  | AAGCAGAAATGAGAATGGTTCTTTCCCCAGTACCCAGAACTTGTGAAGGACGGCTCCAG   | 118  |
| Qy | 1566 | AGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAACACTTT  | 1625 |
| Db | 117  | AGCGTACATCACCTGTGATTCTTTACCTCAGCAACCGAGAGTACTGCAGCAAACATTTT   | 58   |
| Qy | 1626 | CCCTTTGTTAGAAGATCATACTTCAGAAAAATAAACAGATGAAAAAAAAATAGAAGA     | 1682 |
| Db | 57   | CCCTGTGCTAGAAGATCACACTTCAGAAAAATAACACAGATGAAAAAAAAAAAAAAAAA   | 1    |



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Db      362 CCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCACCATATGAAGAAGCC 421
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Qy      2173 ATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTT 2232
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Db      482 AATGCAGCTGCTT CAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAAA 541
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Db      542 GAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATT CAGAAATAGCAAAA 601
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Qy      2353 TTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAA 2412
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Db      602 TTTGAGAAGTCGGTGCTGATCACTGTGAGCTCGTGGATGATTCCTCACCCGAATCTGAA 661
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Qy      2413 CCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCT 2472
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Db      662 CCAGTTGACTTATTTAGTGATGATTCAATTCTGAAGT-CCACANACACAAGAGGAGGCT 720
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Qy      2473 GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTG 2509
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# RESULT 11

CA320618

LOCUS CA320618 777 bp mRNA linear EST 26-NOV-2002

DEFINITION UI-M-FW0-ccb-k-24-0-UI.r1 NIH\_BMAP\_FW0 Mus musculus cDNA clone

IMAGE: 6817393 5', mRNA sequence.

ACCESSION CA320618

VERSION CA320618.1 GI:24538742

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 777)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES

Location/Qualifiers



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| Db | 361  | CTGAGACAGTAAACACAACACAAAATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAG  | 420  |
| Qy | 2564 | GAAAGCCATATTTAGAGTCTTTTTAGCCCAATTTACATAGTACAAAAGATGCTGCATCTA  | 2623 |
| Db | 421  | GAAAGCCATATTTAGAGTCTTTTTAGCCCAATTTACATATTACAAAAGATGCTGCATCTA  | 480  |
| Qy | 2624 | ATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATA | 2683 |
| Db | 481  | ATGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATA  | 540  |
| Qy | 2684 | CTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTG  | 2743 |
| Db | 541  | CTGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTG  | 600  |
| Qy | 2744 | AAACATTTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTTCAGTG  | 2803 |
| Db | 601  | AAACATTTTTCAGATTCTCTCTCATTGAGATAATAGATGAGTTTCCACATTTGTTCAGTG  | 660  |
| Qy | 2804 | CTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAA  | 2863 |
| Db | 661  | CTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAA      | 711  |
| Qy | 2864 | GTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTGCCCTGTG | 2923 |
| Db | 712  | GTGAAATTGCTAATGTCCAGAGCGGNGGCAATTTCGTTGCCTTGCTCAGAATTGCCCTGTG | 771  |
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| Db | 772  | ACCTTT  | 777  |



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Db      301 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTC 360
Qy      2508 TGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGG 2564
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Db      361 TGAGACAGTAACACAACACAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAGG 420
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Db      421 AAAGCCATATTTAGAGTCTTTTTAGCCCAATTTACATATTACAAAAGATGCTGCATCTAA 480
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Qy      2685 TGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGA 2744
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Db      712 TGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGATTG-CCTGTGA 770
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Db      771 CCTTTCTTTTCANG-ATACATATCCTAAAGATGA 802

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RESULT 13

BQ892001

LOCUS BQ892001 951 bp mRNA linear EST 16-AUG-2002

DEFINITION AGENCOURT\_8758347 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6315079  
5', mRNA sequence.

ACCESSION BQ892001

VERSION BQ892001.1 GI:22284015

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 951)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Susan L. Sullivan, PhD.

cDNA Library Preparation: ResGen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13744 row: n column: 08

High quality sequence start: 6

High quality sequence stop: 629.

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unidirectionally. Primer: Oligo dT. Average insert size  
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this  
is a NIH\_MGC Library."  
BASE COUNT 279 a 186 c 222 g 263 t 1 others  
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Query Match 17.6%; Score 659.2; DB 13; Length 951;  
Best Local Similarity 89.3%; Pred. No. 4.1e-94;  
Matches 780; Conservative 0; Mismatches 79; Indels 14; Gaps 6;

Qy 2646 AAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGA 2705  
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Qy 2706 CTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCC 2765  
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Db 71 CTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCAGATTCATCTCC 130  
Qy 2766 GATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTAAAGATGATTCTCTCTAAAT 2825  
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Db 131 CATTGAGATAATAGATGAGTTTCCACATTTGTGCTAGTAAAGATGATTCTCTCT----- 185  
Qy 2826 AGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAG 2885  
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Db 186 ----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAG 241  
Qy 2886 CGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATA 2945  
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Db 242 CGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATA 301  
Qy 2946 TCCTAAAGATGAAGTACATGTTTCTAGATGAATTCTCCGAAAATAGGTCCAGTGATCTAA 3005  
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Db 302 TCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGATCTAA 361  
Qy 3006 GGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCAT 3065  
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Db 362 GGTGCCCTTATTGCTTCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAACAT 421  
Qy 3066 AGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAA 3125  
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|----|------|--|------|
| Db | 422  | AGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAA       | 481  |
| Qy | 3126 | AGAGGACAGATCCCTGTGAGCTGTATTGTCTAGCAGAGCTGAGTAA | 3185 |
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| Db | 482  | AGAGGACAGATCCCTGACAGCTGTATTGTCTAGCAGAGCTGAATA  | 541  |
| Qy | 3186 | CCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT      | 3245 |
|    |      |  |      |
| Db | 542  | CCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT      | 601  |
| Qy | 3246 | GCTGCTGTCTCTGACAGTGTTTCTAGCATTGTCTAGTGTAA      | 3304 |
|    |      |  |      |
| Db | 602  | GCTGCTGTCTCTGACAGTGTTTCTAGCATTGTCTAGTGTAA      | 661  |
| Qy | 3305 | TGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGAT    | 3364 |
|    |      |  |      |
| Db | 662  | TGCTCTCTGTGACTATNCAGCTTAGGATATATAAGGGTGTGAT    | 721  |
| Qy | 3365 | CAGATGAAGGCCA-CCCATTCTAGGGCATATTTAGAACTCTGA    | 3423 |
|    |      |  |      |
| Db | 722  | CAGATGAAGGCCACCCCTTTCTAGGGCATATTTGGGATCTGA     | 781  |
| Qy | 3424 | TTGG-TTCAGAAATACA-GTAATTCTGCTCTTGGTCTATGTGA    | 3480 |
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| Db | 782  | TTGGTTTCAGAAATATAGGAAATTCTGCTCTTGGGCTATGGG     | 841  |
| Qy | 3481 | CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT              | 3513 |
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Seq primer: pYX-5.

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                Site_2: Not I; The library was constructed according
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel. First strand cDNA synthesis was primed with oligo-dT
                primer containing a Not I site. Double strand cDNA was
                size selected according to mRNA size fraction, ligated
                with EcoR I adaptor, digested with NotI and then cloned
                directionally into pYX-Asc vector. The library tag
                sequence located between the Not I site and the polyA tail
                is AGCGAGACAG. This library was created for the University
                Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                Developing Mouse Nervous System', supported by National
                Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                program coordinator."

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Query Match 17.3%; Score 648.6; DB 13; Length 739;  
Best Local Similarity 92.9%; Pred. No. 2e-92;  
Matches 694; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

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| Qy   | 2721 | GGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGA  | 2780 |
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| Db   | 2    | GGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTTCATCTCCCATTGAGATAATAGA  | 61   |
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|      |      |  |      |
| Db   | 62   | TGAGTTTCCACATTTGTCA GTGCTAAAGATGATTCTCCT-----AAGGAGTACAC       | 112  |
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| Qy   | 2841 | TGATCTAGAAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATT | 2900 |
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|      |      |  |      |
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RESULT 15

CA320833

LOCUS CA320833 742 bp mRNA linear EST 26-NOV-2002

DEFINITION UI-M-FW0-ccb-n-23-0-UI.r1 NIH\_BMAP\_FW0 Mus musculus cDNA clone  
 IMAGE: 6817464 5', mRNA sequence.

ACCESSION CA320833

VERSION CA320833.1 GI:24538931

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 742)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

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                                Site\_2: Not I; The library was constructed according  
                                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
                                1996. Denatured RNA was size fractionated on a 1% agarose  
                                gel. First strand cDNA synthesis was primed with oligo-dT  
                                primer containing a Not I site. Double strand cDNA was  
                                size selected according to mRNA size fraction, ligated  
                                with EcoR I adaptor, digested with NotI and then cloned  
                                directionally into pYX-Asc vector. The library tag  
                                sequence located between the Not I site and the polyA tail  
                                is AGCGAGACAG. This library was created for the University  
                                Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
                                Developing Mouse Nervous System', supported by National  
                                Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
                                program coordinator."

BASE COUNT            227 a    149 c    154 g    212 t  
ORIGIN

Query Match                      17.1%;    Score 638.4;    DB 14;    Length 742;  
Best Local Similarity    92.6%;    Pred. No. 8.1e-91;  
Matches 696;    Conservative    0;    Mismatches    46;    Indels    10;    Gaps    2;

Qy            2644    AAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGAT    2703  
                  ||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
Db            1    AATCTGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGAT    60  
  
Qy            2704    GACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCT    2763  
                  |||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
Db            61    GACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCCGATTCATCT    120  
  
Qy            2764    CCGATTGAGATAATAGATGAATTTCCACGTTTGTTCAGTGCTAAAGATGATTCTCCTAAA    2823  
                  ||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
Db            121    CCCATTGAGATAATAGATGAGTTTCCACATTTGTTCAGTGCTAAAGATGATTCTCCT---    177  
  
Qy            2824    TTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAA    2883  
                  |||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
Db            178    -----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAG    231  
  
Qy            2884    AGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATA    2943  
                  |||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
Db            232    AGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACA    291  
  
Qy            2944    TATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCT    3003  
                  |||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
Db            292    TATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTATCT    351

|    |      |   |      |
|----|------|---|------|
| Qy | 3004 | AAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAAACCTCAGACAGAAAATGGGCAGC  | 3063 |
|    |      |   |      |
| Db | 352  | AAGGTGCCCTTATTGCTTCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAAC     | 411  |
| Qy | 3064 | ATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAA ACTTCCTTCTGACACAGAG   | 3123 |
|    |      |   |      |
| Db | 412  | ATAGTTAAACCCAAAGTA CTTACGAAAGAAGCAGAGGAAAAA ACTTCCTTCTGATACAGAG | 471  |
| Qy | 3124 | AAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAACTTCAGTTGTT     | 3183 |
|    |      |   |      |
| Db | 472  | AAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAACTTCAGTTGTT    | 531  |
| Qy | 3184 | GACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTG GTGTTTGGTGCCAGCTTATTC   | 3243 |
|    |      |   |      |
| Db | 532  | GACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG GTGTTTGGTGCCAGCTTATTC   | 591  |
| Qy | 3244 | CTGCTGCTGTCTCTGACAGTGTT CAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCC   | 3303 |
|    |      |   |      |
| Db | 592  | CTGCTGCTGTCTCTGACAGTGTT CAGCATTGTCAGTGTAACGGCCTACATTGCCTTGGCC   | 651  |
| Qy | 3304 | CTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAA    | 3363 |
|    |      |   |      |
| Db | 652  | CTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGAAA    | 711  |
| Qy | 3364 | TCAGATGAAGGCCACCCATT CAGGGCATATTT                               | 3395 |
|    |      |   |      |
| Db | 712  | TCAGATGAAGGCCA- CCATT CAGGGCATATTT                              | 742  |

Search completed: January 23, 2004, 14:46:28  
Job time : 7246.48 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 00:42:43 ; Search time 896.477 Seconds  
(without alignments)  
11264.762 Million cell updates/sec

Title: US-09-830-972-1  
Perfect score: 3741  
Sequence: 1 attgctcgtctggcgcgcg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*  
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19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*  
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25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | % Query |        | Length | DB   | ID       | Description        |                    |
|--------|---------|--------|--------|------|----------|--------------------|--------------------|
|        | No.     | Score  |        |      |          |                    |                    |
| c      | 1       | 3739.4 | 100.0  | 4684 | 21       | AAD011173          | Rat neurite growth |
|        | 2       | 3739.4 | 100.0  | 4684 | 24       | ABN86600           | Rat neurotransmitt |
|        | 3       | 2343.6 | 62.6   | 4053 | 22       | AAS09453           | Human cDNA encodin |
|        | 4       | 2343.6 | 62.6   | 4632 | 24       | ABV94680           | Human pancreatic c |
|        | 5       | 2333.2 | 62.4   | 4093 | 21       | AAA23454           | cDNA encoding huma |
|        | 6       | 2323.8 | 62.1   | 4822 | 24       | ABS70449           | Human bone remodel |
|        | 7       | 2297.4 | 61.4   | 4698 | 25       | ABX34563           | Human mddt cDNA SE |
|        | 8       | 2289.2 | 61.2   | 3579 | 21       | AAZ56886           | Human MAGI polypep |
|        | 9       | 2289.2 | 61.2   | 3579 | 22       | AAF90324           | Human NOGO-A cDNA. |
|        | 10      | 2289.2 | 61.2   | 3579 | 24       | ABN86601           | Human neurotransmi |
|        | 11      | 2289.2 | 61.2   | 3579 | 24       | ABK90134           | DNA encoding human |
|        | 12      | 1869.8 | 50.0   | 3833 | 21       | AAD01174           | Bovine neurite gro |
|        | 13      | 1411.2 | 37.7   | 2386 | 19       | AAV30920           | Human secreted pro |
|        | 14      | 1408   | 37.6   | 2386 | 22       | AAF98399           | Human cDNA clone B |
|        | 15      | 1088.8 | 29.1   | 1980 | 22       | AAI98079           | Human neuroblastom |
|        | 16      | 564    | 15.1   | 1568 | 21       | AAD01175           | Rat neurite growth |
|        | 17      | 503.2  | 13.5   | 1758 | 22       | AAF32725           | Human secreted pro |
|        | 18      | 497.4  | 13.3   | 600  | 22       | AAF90323           | Human NOGO-C cDNA. |
|        | 19      | 497.4  | 13.3   | 770  | 21       | AAA72983           | Human NSPH encodin |
|        | 20      | 497.4  | 13.3   | 799  | 19       | AAV23695           | Human NSPLP protei |
|        | 21      | 497.4  | 13.3   | 1122 | 21       | AAZ56888           | Human MAGI polypep |
|        | 22      | 497.4  | 13.3   | 1122 | 22       | AAF90325           | Human NOGO-B cDNA. |
|        | 23      | 497.4  | 13.3   | 1213 | 20       | AAX04379           | Human secreted pro |
|        | 24      | 497.4  | 13.3   | 1216 | 24       | ABA05903           | Human RTN4B encodi |
|        | 25      | 497.4  | 13.3   | 2052 | 24       | ABK90133           | DNA encoding human |
|        | 26      | 497.4  | 13.3   | 2235 | 24       | ABV94681           | Human pancreatic c |
|        | 27      | 497.4  | 13.3   | 2240 | 21       | AAC64406           | Human Nogo B nucle |
|        | 28      | 495.8  | 13.3   | 991  | 20       | AAX97587           | Extended human sec |
|        | 29      | 495.8  | 13.3   | 1610 | 21       | AAZ36230           | cDNA encoding a bo |
|        | 30      | 495.8  | 13.3   | 1694 | 22       | AAK94408           | Human full-length  |
|        | 31      | 483.6  | 12.9   | 868  | 21       | AAZ56887           | Human MAGI polypep |
|        | 32      | 475    | 12.7   | 1798 | 24       | ABK90135           | DNA encoding human |
|        | 33      | 468    | 12.5   | 1514 | 24       | ABK34580           | Human cDNA for nov |
|        | 34      | 391.6  | 10.5   | 1683 | 22       | AAD08386           | Human secreted pro |
|        | 35      | 375.6  | 10.0   | 422  | 25       | ABX43312           | Bovine EST associa |
|        | 36      | 374    | 10.0   | 422  | 25       | ABX46402           | Bovine EST associa |
|        | 37      | 323    | 8.6    | 460  | 20       | AAV87027           | EST clone BG160.   |
|        | 38      | 322.4  | 8.6    | 389  | 25       | ABX39989           | Bovine EST associa |
|        | 39      | 316.2  | 8.5    | 615  | 22       | AAK93939           | Human cDNA clone r |
|        | 40      | 302.6  | 8.1    | 423  | 25       | ABX43927           | Bovine EST associa |
| 41     | 299     | 8.0    | 562    | 22   | AAK93574 | Human cDNA clone r |                    |
| 42     | 278.8   | 7.5    | 742    | 22   | AAI96236 | Human neuroblastom |                    |
| 43     | 266.4   | 7.1    | 668    | 24   | ABL89601 | Human polynucleoti |                    |
| 44     | 258.2   | 6.9    | 495    | 22   | AAK92091 | Human cDNA 5'-end  |                    |
| 45     | 253.2   | 6.8    | 3202   | 19   | AAX75770 | Human neuroendocri |                    |

# ALIGNMENTS

RESULT 1

AAD01173

ID AAD01173 standard; cDNA; 4684 BP.

XX

AC AAD01173;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A cDNA.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 253..3744

FT /\*tag= a

FT /product= "Nogo A"

FT /transl\_except= (pos:1462..1464, aa:Ile)

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

DR P-PSDB; AAY71310.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic  
 PT disorders of the central nervous system and inducing regeneration of  
 PT neurons -

XX

PS Claim 26; Fig 2A; 122pp; English.

XX

CC The present sequence is a cDNA encoding rat Nogo A protein which is a  
 CC potent neural cell growth inhibitor and is free of all central nervous  
 CC system (CNS) myelin material with which it is natively associated.  
 CC The present sequence was generated by fusing RO18U37-3, R1-3U21 cDNA  
 CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord  
 CC library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte  
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory  
 CC activity are used in the treatment of neoplastic disease of the CNS



CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve  
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
CC promote Nogo activity can be used to treat or prevent hyperproliferative  
CC or benign dysproliferative disorders e.g. psoriasis and tissue  
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to  
CC inhibit production of Nogo protein to induce regeneration of neurons or  
CC to promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired.  
CC The animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which  
CC can treat or prevent disorders or diseases of the CNS.  
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29  
CC in disclosure of the specification. However the specification does not  
CC include sequences for these SEQ ID numbers.

XX

SEQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 other;

Query Match 100.0%; Score 3739.4; DB 21; Length 4684;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | ATTGCTCGTCTGGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG     | 60  |
|    |     |   |     |
| Db | 1   | ATTGCTCGTCTGGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG     | 60  |
| Qy | 61  | ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT  | 120 |
|    |     |   |     |
| Db | 61  | ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT  | 120 |
| Qy | 121 | CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA | 180 |
|    |     |   |     |
| Db | 121 | CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA | 180 |
| Qy | 181 | ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC  | 240 |
|    |     |   |     |
| Db | 181 | ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC  | 240 |
| Qy | 241 | GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC  | 300 |
|    |     |   |     |
| Db | 241 | GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC  | 300 |
| Qy | 301 | CCGCCCCGGCCTCCGCCCCCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG  | 360 |
|    |     |   |     |
| Db | 301 | CCGCCCCGGCCTCCGCCCCCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG  | 360 |
| Qy | 361 | GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG  | 420 |
|    |     |   |     |
| Db | 361 | GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG  | 420 |
| Qy | 421 | CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCGCCGCCGCCGCCG  | 480 |
|    |     |   |     |
| Db | 421 | CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCGCCGCCGCCGCCG  | 480 |
| Qy | 481 | CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC   | 540 |
|    |     |   |     |

|    |      |   |      |
|----|------|---|------|
| Db | 481  | CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC   | 540  |
| Qy | 541  | GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG  | 600  |
|    |      |   |      |
| Db | 541  | GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG  | 600  |
| Qy | 601  | CCATCCCTGCCGCCCCTGCCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT    | 660  |
|    |      |   |      |
| Db | 601  | CCATCCCTGCCGCCCCTGCCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT    | 660  |
| Qy | 661  | CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCCCGCG    | 720  |
|    |      |   |      |
| Db | 661  | CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCCCGCG    | 720  |
| Qy | 721  | CCCCCTTCCACGCCGCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCCTT   | 780  |
|    |      |   |      |
| Db | 721  | CCCCCTTCCACGCCGCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCCTT   | 780  |
| Qy | 781  | TTTGCTCTTCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAATTATGGAT    | 840  |
|    |      |   |      |
| Db | 781  | TTTGCTCTTCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAATTATGGAT    | 840  |
| Qy | 841  | TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCCTG | 900  |
|    |      |   |      |
| Db | 841  | TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCCTG | 900  |
| Qy | 901  | CTTGAAACTGCTGCCTCTCTTCTTCTCTATCTCCTCTCTCAACTGTTTCTTTAAAGAA    | 960  |
|    |      |   |      |
| Db | 901  | CTTGAAACTGCTGCCTCTCTTCTTCTCTATCTCCTCTCTCAACTGTTTCTTTAAAGAA    | 960  |
| Qy | 961  | CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAAACT   | 1020 |
|    |      |   |      |
| Db | 961  | CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAAACT   | 1020 |
| Qy | 1021 | TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT  | 1080 |
|    |      |   |      |
| Db | 1021 | TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT  | 1080 |
| Qy | 1081 | TTAGCAGAAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA | 1140 |
|    |      |   |      |
| Db | 1081 | TTAGCAGAAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA | 1140 |
| Qy | 1141 | AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA | 1200 |
|    |      |   |      |
| Db | 1141 | AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA | 1200 |
| Qy | 1201 | GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT  | 1260 |
|    |      |   |      |
| Db | 1201 | GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT  | 1260 |
| Qy | 1261 | AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG  | 1320 |
|    |      |   |      |
| Db | 1261 | AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG  | 1320 |
| Qy | 1321 | TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG  | 1380 |
|    |      |   |      |
| Db | 1321 | TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG  | 1380 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1381 | GAAGTGAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA   | 1440 |
| Db | 1381 | GAAGTGAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA   | 1440 |
| Qy | 1441 | AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAGGAT    | 1500 |
| Db | 1441 | AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAGGAT    | 1500 |
| Qy | 1501 | AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGACAGC    | 1560 |
| Db | 1501 | AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGACAGC    | 1560 |
| Qy | 1561 | TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC  | 1620 |
| Db | 1561 | TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC  | 1620 |
| Qy | 1621 | ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAAAGATGAAAAAAAAATAGAA   | 1680 |
| Db | 1621 | ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAAAGATGAAAAAAAAATAGAA   | 1680 |
| Qy | 1681 | GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT  | 1740 |
| Db | 1681 | GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT  | 1740 |
| Qy | 1741 | GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT  | 1800 |
| Db | 1741 | GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT  | 1800 |
| Qy | 1801 | GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAAGGAAGCATGT | 1860 |
| Db | 1801 | GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAAGGAAGCATGT | 1860 |
| Qy | 1861 | GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG  | 1920 |
| Db | 1861 | GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG  | 1920 |
| Qy | 1921 | GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA   | 1980 |
| Db | 1921 | GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA   | 1980 |
| Qy | 1981 | TTTGAGGAAGCTGAAGCAACTCCGTACCAGTTTGCCTGATATTGTTATGGAAGCACCA    | 2040 |
| Db | 1981 | TTTGAGGAAGCTGAAGCAACTCCGTACCAGTTTGCCTGATATTGTTATGGAAGCACCA    | 2040 |
| Qy | 2041 | TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTATCCCCACTG   | 2100 |
| Db | 2041 | TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTATCCCCACTG   | 2100 |
| Qy | 2101 | GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA   | 2160 |
| Db | 2101 | GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA   | 2160 |
| Qy | 2161 | TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG  | 2220 |
| Db | 2161 | TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG  | 2220 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2221 | CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT  | 2280 |
|    |      |  |      |
| Db | 2221 | CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT  | 2280 |
| Qy | 2281 | GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA   | 2340 |
|    |      |  |      |
| Db | 2281 | GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA   | 2340 |
| Qy | 2341 | GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA  | 2400 |
|    |      |  |      |
| Db | 2341 | GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA  | 2400 |
| Qy | 2401 | CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACA  | 2460 |
|    |      |  |      |
| Db | 2401 | CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACA  | 2460 |
| Qy | 2461 | CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC   | 2520 |
|    |      |  |      |
| Db | 2461 | CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC   | 2520 |
| Qy | 2521 | CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG   | 2580 |
|    |      |  |      |
| Db | 2521 | CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG   | 2580 |
| Qy | 2581 | TCTTTTCAGCCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG  | 2640 |
|    |      |  |      |
| Db | 2581 | TCTTTTCAGCCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG  | 2640 |
| Qy | 2641 | ACCAAAAAGGAGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT | 2700 |
|    |      |  |      |
| Db | 2641 | ACCAAAAAGGAGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT | 2700 |
| Qy | 2701 | GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA   | 2760 |
|    |      |  |      |
| Db | 2701 | GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA   | 2760 |
| Qy | 2761 | TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTTCAGTGCCTAAAGATGATTCTCCT  | 2820 |
|    |      |  |      |
| Db | 2761 | TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTTCAGTGCCTAAAGATGATTCTCCT  | 2820 |
| Qy | 2821 | AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC   | 2880 |
|    |      |  |      |
| Db | 2821 | AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC   | 2880 |
| Qy | 2881 | CAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT  | 2940 |
|    |      |  |      |
| Db | 2881 | CAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT  | 2940 |
| Qy | 2941 | ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA   | 3000 |
|    |      |  |      |
| Db | 2941 | ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA   | 3000 |
| Qy | 3001 | TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC   | 3060 |
|    |      |  |      |
| Db | 3001 | TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC   | 3060 |
| Qy | 3061 | AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA   | 3120 |

|    |      |  |      |
|----|------|--|------|
| Db | 3061 | <br>AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA   | 3120 |
| Qy | 3121 | GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT       | 3180 |
| Db | 3121 | <br>GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT   | 3180 |
| Qy | 3181 | GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA       | 3240 |
| Db | 3181 | <br>GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTA   | 3240 |
| Qy | 3241 | TTCCTGCTGCTGTCTCTGACAGTGTTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG     | 3300 |
| Db | 3241 | <br>TTCCTGCTGCTGTCTCTGACAGTGTTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG | 3300 |
| Qy | 3301 | GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG       | 3360 |
| Db | 3301 | <br>GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG   | 3360 |
| Qy | 3361 | AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG      | 3420 |
| Db | 3361 | <br>AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG  | 3420 |
| Qy | 3421 | GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAGAA      | 3480 |
| Db | 3421 | <br>GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAGAA  | 3480 |
| Qy | 3481 | CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCACTGTTGATG       | 3540 |
| Db | 3481 | <br>CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCACTGTTGATG   | 3540 |
| Qy | 3541 | TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG       | 3600 |
| Db | 3541 | <br>TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG   | 3600 |
| Qy | 3601 | ATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT        | 3660 |
| Db | 3601 | <br>ATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT    | 3660 |
| Qy | 3661 | CTAGGACTTGCAAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT      | 3720 |
| Db | 3661 | <br>CTAGGACTTGCAAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT  | 3720 |
| Qy | 3721 | GGATTGAAGCGCAAAGCAGAT  | 3741 |
| Db | 3721 | <br>GGATTGAAGCGCAAAGCAGAT  | 3741 |

RESULT 2

ABN86600

ID ABN86600 standard; DNA; 4684 BP.

XX

AC ABN86600;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo encoding DNA.

XX  
 KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; gene; ds.  
 XX  
 OS Rattus norvegicus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 253..3744  
 FT /\*tag= a  
 FT /product= "Nogo-A"  
 XX  
 PN US2002072493-A1.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 28-JUN-2001; 2001US-0893348.  
 XX  
 PR 19-MAY-1998; 98IL-0124500.  
 PR 21-JUL-1998; 98WO-US14715.  
 PR 22-DEC-1998; 98US-0218277.  
 PR 19-MAY-1999; 99US-0314161.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR P-PSDB; ABB81074, ABB81076, ABB81077.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in  
 PT the central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides -  
 XX  
 PS Disclosure; Page 40-44; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease  
 CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such



|    |      |   |      |
|----|------|---|------|
| Db | 541  | <br>GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG  | 600  |
| Qy | 601  | <br>CCATCCCTGCCGCCCCTGCCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT     | 660  |
| Db | 601  | <br>CCATCCCTGCCGCCCCTGCCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT     | 660  |
| Qy | 661  | <br>CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAGCCCCCGCG     | 720  |
| Db | 661  | <br>CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAGCCCCCGCG     | 720  |
| Qy | 721  | <br>CCCCCTTCCACGCCGCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT    | 780  |
| Db | 721  | <br>CCCCCTTCCACGCCGCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT    | 780  |
| Qy | 781  | <br>TTTGCTCTTCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT   | 840  |
| Db | 781  | <br>TTTGCTCTTCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT   | 840  |
| Qy | 841  | <br>TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG  | 900  |
| Db | 841  | <br>TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG  | 900  |
| Qy | 901  | <br>CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA  | 960  |
| Db | 901  | <br>CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA  | 960  |
| Qy | 961  | <br>CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAAACT   | 1020 |
| Db | 961  | <br>CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAAACT   | 1020 |
| Qy | 1021 | <br>TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT  | 1080 |
| Db | 1021 | <br>TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT  | 1080 |
| Qy | 1081 | <br>TTAGCAGAATTTTCAGAAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA | 1140 |
| Db | 1081 | <br>TTAGCAGAATTTTCAGAAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA | 1140 |
| Qy | 1141 | <br>AAAGGAGAGTCAGCCATATTAGTAGAAAACTAAGGAAGAAGTAATTGTGAGGAGTAAA    | 1200 |
| Db | 1141 | <br>AAAGGAGAGTCAGCCATATTAGTAGAAAACTAAGGAAGAAGTAATTGTGAGGAGTAAA    | 1200 |
| Qy | 1201 | <br>GACAAAGAGGATTTAGTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT   | 1260 |
| Db | 1201 | <br>GACAAAGAGGATTTAGTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT   | 1260 |
| Qy | 1261 | <br>AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATG  | 1320 |
| Db | 1261 | <br>AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATG  | 1320 |
| Qy | 1321 | <br>TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG  | 1380 |
| Db | 1321 | <br>TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG  | 1380 |
| Qy | 1381 | <br>GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA  | 1440 |



|    |      |   |      |
|----|------|---|------|
| Db | 1381 | GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA  | 1440 |
| Qy | 1441 | AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGAT   | 1500 |
|    |      |   |      |
| Db | 1441 | AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGAT   | 1500 |
| Qy | 1501 | AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC | 1560 |
|    |      |   |      |
| Db | 1501 | AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC | 1560 |
| Qy | 1561 | TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC  | 1620 |
|    |      |   |      |
| Db | 1561 | TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC  | 1620 |
| Qy | 1621 | ACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA | 1680 |
|    |      |   |      |
| Db | 1621 | ACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA | 1680 |
| Qy | 1681 | GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCCTT | 1740 |
|    |      |   |      |
| Db | 1681 | GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCCTT | 1740 |
| Qy | 1741 | GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT  | 1800 |
|    |      |   |      |
| Db | 1741 | GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT  | 1800 |
| Qy | 1801 | GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT  | 1860 |
|    |      |   |      |
| Db | 1801 | GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT  | 1860 |
| Qy | 1861 | GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGAAGTGT | 1920 |
|    |      |   |      |
| Db | 1861 | GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGAAGTGT | 1920 |
| Qy | 1921 | GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA   | 1980 |
|    |      |   |      |
| Db | 1921 | GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA   | 1980 |
| Qy | 1981 | TTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCACCA  | 2040 |
|    |      |   |      |
| Db | 1981 | TTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCACCA  | 2040 |
| Qy | 2041 | TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG  | 2100 |
|    |      |   |      |
| Db | 2041 | TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG  | 2100 |
| Qy | 2101 | GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA   | 2160 |
|    |      |   |      |
| Db | 2101 | GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA   | 2160 |
| Qy | 2161 | TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG  | 2220 |
|    |      |   |      |
| Db | 2161 | TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG  | 2220 |
| Qy | 2221 | CCTGAAAGTTTAAATGCAGCTGTTTCAAGAAACAGAAGCTCCTTATATATCCATTGCGTGT | 2280 |
|    |      |   |      |
| Db | 2221 | CCTGAAAGTTTAAATGCAGCTGTTTCAAGAAACAGAAGCTCCTTATATATCCATTGCGTGT | 2280 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2281 | GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA   | 2340 |
|    |      |  |      |
| Db | 2281 | GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA   | 2340 |
| Qy | 2341 | GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGAGGATTCTCTCA   | 2400 |
|    |      |  |      |
| Db | 2341 | GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGAGGATTCTCTCA   | 2400 |
| Qy | 2401 | CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTTCCTGAAGTCCCACAAACA | 2460 |
|    |      |  |      |
| Db | 2401 | CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTTCCTGAAGTCCCACAAACA | 2460 |
| Qy | 2461 | CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC   | 2520 |
|    |      |  |      |
| Db | 2461 | CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC   | 2520 |
| Qy | 2521 | CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG   | 2580 |
|    |      |  |      |
| Db | 2521 | CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG   | 2580 |
| Qy | 2581 | TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG   | 2640 |
|    |      |  |      |
| Db | 2581 | TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG   | 2640 |
| Qy | 2641 | ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT  | 2700 |
|    |      |  |      |
| Db | 2641 | ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT  | 2700 |
| Qy | 2701 | GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA   | 2760 |
|    |      |  |      |
| Db | 2701 | GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA   | 2760 |
| Qy | 2761 | TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTGCTAAAGATGATTCTCCT     | 2820 |
|    |      |  |      |
| Db | 2761 | TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTGCTAAAGATGATTCTCCT     | 2820 |
| Qy | 2821 | AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC   | 2880 |
|    |      |  |      |
| Db | 2821 | AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC   | 2880 |
| Qy | 2881 | CAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT  | 2940 |
|    |      |  |      |
| Db | 2881 | CAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT  | 2940 |
| Qy | 2941 | ATATATCCTAAAGATGAAGTACATGTTTTAGATGAATTCTCCGAAAATAGGTCCAGTGTA   | 3000 |
|    |      |  |      |
| Db | 2941 | ATATATCCTAAAGATGAAGTACATGTTTTAGATGAATTCTCCGAAAATAGGTCCAGTGTA   | 3000 |
| Qy | 3001 | TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC   | 3060 |
|    |      |  |      |
| Db | 3001 | TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC   | 3060 |
| Qy | 3061 | AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA   | 3120 |
|    |      |  |      |
| Db | 3061 | AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA   | 3120 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3121 | GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT   | 3180 |
|    |      |  |      |
| Db | 3121 | GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT   | 3180 |
| Qy | 3181 | GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA  | 3240 |
|    |      |  |      |
| Db | 3181 | GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA  | 3240 |
| Qy | 3241 | TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTG  | 3300 |
|    |      |  |      |
| Db | 3241 | TTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTG  | 3300 |
| Qy | 3301 | GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG   | 3360 |
|    |      |  |      |
| Db | 3301 | GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG   | 3360 |
| Qy | 3361 | AAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAACTCTGAAGTTGCTATATCAGAG  | 3420 |
|    |      |  |      |
| Db | 3361 | AAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAACTCTGAAGTTGCTATATCAGAG  | 3420 |
| Qy | 3421 | GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAA | 3480 |
|    |      |  |      |
| Db | 3421 | GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAA | 3480 |
| Qy | 3481 | CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTGATG     | 3540 |
|    |      |  |      |
| Db | 3481 | CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTGATG     | 3540 |
| Qy | 3541 | TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG   | 3600 |
|    |      |  |      |
| Db | 3541 | TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG   | 3600 |
| Qy | 3601 | ATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT    | 3660 |
|    |      |  |      |
| Db | 3601 | ATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT    | 3660 |
| Qy | 3661 | CTAGGACTTGCAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT    | 3720 |
|    |      |  |      |
| Db | 3661 | CTAGGACTTGCAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT    | 3720 |
| Qy | 3721 | GGATTGAAGCGCAAAGCAGAT  | 3741 |
|    |      |  |      |
| Db | 3721 | GGATTGAAGCGCAAAGCAGAT  | 3741 |

RESULT 3

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

XX

AC AAS09453;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human cDNA encoding the Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;  
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
 KW Krabbe's disease; AB020693; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 135..3713  
 FT /\*tag= a  
 FT /product= "Nogo protein"  
 XX  
 PN WO200151520-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 12-JAN-2001; 2001WO-US01041.  
 XX  
 PR 12-JAN-2000; 2000US-0175707.  
 PR 26-MAY-2000; 2000US-0207366.  
 PR 29-SEP-2000; 2000US-0236378.  
 XX  
 PA (UYA ) UNIV YALE.  
 XX  
 PI Strittmatter SM;  
 XX  
 DR WPI; 2001-442138/47.  
 DR P-PSDB; AAU09453.  
 XX  
 PT Novel Nogo receptor protein useful for identifying modulator of Nogo  
 PT protein or Nogo receptor protein, which is useful for treating central  
 PT nervous system disorders -  
 XX  
 PS Example 1; Page 95-100; 109pp; English.  
 XX  
 CC The sequence (Genbank accession number AB0202693) encodes the human Nogo  
 CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention  
 CC relates to the use of the nogoreceptor, nogo protein, their nucleic  
 CC acids, vectors expressing them and antibodies against them, to isolate  
 CC agents which block nogo receptor mediated axonal growth. The agent is  
 CC useful for treating a central nervous system disorder which is a result  
 CC of cranial or cerebral trauma, spinal cord injury, stroke or a  
 CC demyelinating disease selected from multiple sclerosis, monophasis  
 CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,  
 CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,  
 CC adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,  
 CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,  
 CC viral infection and Krabbe's disease.  
 XX  
 SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 other;

Query Match 62.6%; Score 2343.6; DB 22; Length 4053;  
 Best Local Similarity 81.3%; Pred. No. 0;  
 Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 134 | CACGACTCGGCCTGCCTGCCCTGCCCAGTCTTGGCCCAACCCCCACAACCGCCCGCGACT   | 193 |
| Db | 16  | CTCGGCTCAGTCGGCCCAGCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT    | 75  |
| Qy | 194 | CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC   | 252 |
| Db | 76  | CTGAGACGCGGCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC    | 134 |
| Qy | 253 | ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCT    | 312 |
| Db | 135 | ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCTCGGACAGCCCAACCCGCGCCG | 191 |
| Qy | 313 | CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG   | 372 |
| Db | 192 | CAGCCCGCGTTCAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG    | 248 |
| Qy | 373 | GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG   | 432 |
| Db | 249 | GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG   | 308 |
| Qy | 433 | CCCGCAGCCGGGCTGTCCGCACTGCGGTGC-----CGCCCGCCGCCCGCGCCGCTG       | 486 |
| Db | 309 | CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCGCGCGGCGCGCCCTG      | 368 |
| Qy | 487 | CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCGCGGGCCGCTGCCGGCCGCGCCC     | 546 |
| Db | 369 | ATGGACTTCGGAATGACTTCGTGCGCGCGGCGCCCGGGGACCCCTGCCGCGCGCTCCC     | 428 |
| Qy | 547 | CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC       | 597 |
| Db | 429 | CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTCGTCCGCTGCC     | 488 |
| Qy | 598 | GCGCCATCCCTGCCGCCGCTGCCGCACTCTGCCCTCCAAGCTCCCAGAGGACGACGAG     | 657 |
| Db | 489 | GCGCCATCCCCGCTGTCTGTCTGCCGCACTCTGCCCTCCAAGCTCCCTGAGGACGACGAG   | 548 |
| Qy | 658 | CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG-----     | 711 |
| Db | 549 | CCTCCGGCCCCGGCCTCCCCCTCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG    | 608 |
| Qy | 712 | -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC                   | 750 |
| Db | 609 | TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCAAGCGC     | 668 |
| Qy | 751 | AGGGGCTCC---GGCTCAGTGGATGAGACCTTTTTTGCTCTTCTGCTGCATCTGAGCCT    | 807 |
| Db | 669 | AGGGGCTCCTCGGGCTCAGTGGATGAGACCTTTTTTGCTCTTCTGCTGCATCTGAGCCT    | 728 |
| Qy | 808 | GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT    | 867 |
| Db | 729 | GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT   | 785 |
| Qy | 868 | TCGTCTGGTCAAGAGGATTTCCCATCTGTCTCTGCTTGAACTGCTGCCTCTCTTCTTCT    | 927 |
| Db | 786 | TCGGCTGGTCAAGAGGATTTCCCATCTGTCTCTGCTTGAACTGCTGCTTCTCTTCTTCT    | 845 |
| Qy | 928 | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGTTAACTTATCAGCA   | 987 |

|    |      |  |      |
|----|------|--|------|
| Db | 846  | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA   | 905  |
| Qy | 988  | GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA    | 1047 |
| Db | 906  | GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA   | 965  |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT   | 1107 |
| Db | 966  | GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC | 1025 |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA   | 1167 |
| Db | 1026 | TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA   | 1085 |
| Qy | 1168 | AACACTAAGGAAGAAGTAAATTGTGAGGAGTAAA--GACAAAGAGGATTTAGTTTGTAGT   | 1224 |
| Db | 1086 | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT   | 1145 |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC             | 1269 |
| Db | 1146 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT   | 1205 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA   | 1329 |
| Db | 1206 | GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAA  | 1265 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA   | 1389 |
| Db | 1266 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA   | 1325 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG          | 1437 |
| Db | 1326 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG   | 1382 |
| Qy | 1438 | GAAAGTAAAGTGGACAGAAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG   | 1497 |
| Db | 1383 | GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA    | 1442 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACC'TGTGAAGGAC   | 1557 |
| Db | 1443 | GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT   | 1502 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA   | 1614 |
| Db | 1503 | CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA    | 1562 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA    | 1674 |
| Db | 1563 | ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA    | 1622 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT   | 1731 |
| Db | 1623 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC    | 1682 |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA   | 1791 |

|    |      |   |      |
|----|------|---|------|
| Db | 1683 | CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAACAGATAAATTTAACA  | 1742 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG   | 1851 |
| Db | 1743 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG    | 1802 |
| Qy | 1852 | GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA    | 1911 |
| Db | 1803 | GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA    | 1862 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT     | 1971 |
| Db | 1863 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT    | 1922 |
| Qy | 1972 | TGCCCATCATTGTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG   | 2031 |
| Db | 1923 | TGCCCATCATTGTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTGCCTGACATTGTTATG    | 1982 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA    | 2091 |
| Db | 1983 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA    | 2042 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAAC   | 2151 |
| Db | 2043 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAAAC    | 2099 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA    | 2208 |
| Db | 2100 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA     | 2159 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA    | 2268 |
| Db | 2160 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA    | 2219 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC   | 2328 |
| Db | 2220 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGATTTTC    | 2279 |
| Qy | 2329 | TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG    | 2388 |
| Db | 2280 | TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT    | 2339 |
| Qy | 2389 | GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA | 2448 |
| Db | 2340 | GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC   | 2399 |
| Qy | 2449 | GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A      | 2502 |
| Db | 2400 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA    | 2459 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA    | 2562 |
| Db | 2460 | TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAAGTCACTGCTTTGCCACCTGAGGGA   | 2519 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA    | 2619 |
| Db | 2520 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTATGATAACACAAAAGATACCTTGTTA   | 2579 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2620 | TCTAATGACATTCCAAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAAATGGAAGAGTTT | 2679 |
| Db | 2580 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC   | 2639 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA    | 2739 |
| Db | 2640 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA    | 2699 |
| Qy | 2740 | AGTGAAACATTTTCAGATTCACTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC      | 2799 |
| Db | 2700 | ACTGAAACGTTTTCAGATTCACTCCAATTGAAATTATAGATGAGTTCCTTACATTGATC     | 2759 |
| Qy | 2800 | AGTGCTAAAGATGATTC--TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC     | 2856 |
| Db | 2760 | AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC     | 2819 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGAGATTGCTTGCCTTGCTTAGAATTG     | 2916 |
| Db | 2820 | CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTGCTTGCCTTGACAGAAATTG    | 2879 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA     | 2970 |
| Db | 2880 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA    | 2939 |
| Qy | 2971 | GATGAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTC     | 3030 |
| Db | 2940 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT    | 2999 |
| Qy | 3031 | TCTGCTTTGGAACTTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA    | 3090 |
| Db | 3000 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTAAG     | 3059 |
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA    | 3150 |
| Db | 3060 | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA    | 3119 |
| Qy | 3151 | TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG    | 3210 |
| Db | 3120 | TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG    | 3179 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC   | 3270 |
| Db | 3180 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTATTGACAGTATTGAGC   | 3239 |
| Qy | 3271 | ATTGTGAGTGTAAACGGCCTACATTGCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGG    | 3330 |
| Db | 3240 | ATTGTGAGCGTAAACAGCCTACATTGCCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGG   | 3299 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA    | 3390 |
| Db | 3300 | ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA    | 3359 |
| Qy | 3391 | TATTTAGAACTGGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT   | 3450 |
| Db | 3360 | TATCTGGAATCTGGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAATACAGTAATTCTGCT  | 3419 |



|    |      |   |      |
|----|------|---|------|
| Qy | 3451 | CTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA | 3510 |
|    |      |   |      |
| Db | 3420 | CTTGGTCATGTGAACAGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA  | 3479 |
| Qy | 3511 | GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTTC | 3570 |
|    |      |   |      |
| Db | 3480 | GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT  | 3539 |
| Qy | 3571 | AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT  | 3630 |
|    |      |   |      |
| Db | 3540 | AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT  | 3599 |
| Qy | 3631 | GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT  | 3690 |
|    |      |   |      |
| Db | 3600 | GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT  | 3659 |
| Qy | 3691 | GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA            | 3740 |
|    |      |   |      |
| Db | 3660 | GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA            | 3709 |

RESULT 4

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

XX

AC ABV94680;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW cytostatic; tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

XX

PD 08-AUG-2002.

XX

PF 30-JAN-2002; 2002WO-US02781.

XX

PR 30-JAN-2001; 2001US-265305P.

PR 31-JAN-2001; 2001US-265682P.

PR 09-FEB-2001; 2001US-267568P.

PR 21-MAR-2001; 2001US-278651P.

PR 28-APR-2001; 2001US-287112P.

PR 16-MAY-2001; 2001US-291631P.

PR 12-JUL-2001; 2001US-305484P.

PR 20-AUG-2001; 2001US-313999P.

PR 27-NOV-2001; 2001US-333626P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX

DR WPI; 2002-627435/67.

XX

PT

XX

XX

CC

CC

SQ

9

 $Q_Y$ 

Qy

Qy

Qy

Qy

Qy

Qy 487 CTGGACTTCAGCAGCGACTCGGTGCCCGCCCGCGCCCGCGGGCCGCTGCCCGCCCGCGCCC 546  
Db 376 ATGGACTTCGGAATGACTTCGTGCCGCCGCGCCCGGGGACCCCTGCCCGCCGCTCCC 435

Qy 547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597  
Db 436 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 495

Qy 598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657  
Db 496 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCCTGCCCTCCAAGCTCCCTGAGGACGACGAG 555

Qy 658 CCTCCGCGCAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711  
Db 556 CCTCCGCGCCCGGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 615

Qy 712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750  
Db 616 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC 675

Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT 807  
Db 676 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT 735

Qy 808 GTGATACCCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867  
Db 736 GTGATACGCTCCTCTGCAGAAA--TATGGAATTGAAGGAGCAGCCAGGTAACACTATT 792

Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTTCTGCTTGAAGTCTGCTCTCTTCTTCT 927  
Db 793 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTTCTGCTTGAAGTCTGCTCTCTTCTTCT 852

Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987  
Db 853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTGTCAACA 912

Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047  
Db 913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972

Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107  
Db 973 GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1032

Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167  
Db 1033 TCAGAAATGGGATCATCGTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1092

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA--GACAAAGAGGATTTAGTTTGTAGT 1224  
Db 1093 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1152

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
Db 1153 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1212

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTGAGTAGTA 1322

|    |      |   |      |
|----|------|---|------|
| Db | 1213 | GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA  | 1272 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA  | 1389 |
| Db | 1273 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA  | 1332 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG         | 1437 |
| Db | 1333 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG  | 1389 |
| Qy | 1438 | GAAAGTAAAGTGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG    | 1497 |
| Db | 1390 | GAAAGTAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAAAAA  | 1449 |
| Qy | 1498 | GATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC  | 1557 |
| Db | 1450 | GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT  | 1509 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA  | 1614 |
| Db | 1510 | CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA  | 1569 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA  | 1674 |
| Db | 1570 | ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA  | 1629 |
| Qy | 1675 | ATAGAAGAAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT | 1731 |
| Db | 1630 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC  | 1689 |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA  | 1791 |
| Db | 1690 | CCTTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA | 1749 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG  | 1851 |
| Db | 1750 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG  | 1809 |
| Qy | 1852 | GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA  | 1911 |
| Db | 1810 | GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA  | 1869 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT   | 1971 |
| Db | 1870 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT  | 1929 |
| Qy | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATG   | 2031 |
| Db | 1930 | TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGCCTGACATTGTTATG   | 1989 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA  | 2091 |
| Db | 1990 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA  | 2049 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC  | 2151 |

|    |      |   |      |
|----|------|---|------|
| Db | 2050 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAAC | 2106 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA  | 2208 |
| Db | 2107 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA  | 2166 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA | 2268 |
| Db | 2167 | GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA   | 2226 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC | 2328 |
| Db | 2227 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC | 2286 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG | 2388 |
| Db | 2287 | TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT | 2346 |
| Qy | 2389 | GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA | 2448 |
| Db | 2347 | GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC  | 2406 |
| Qy | 2449 | GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A   | 2502 |
| Db | 2407 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA  | 2466 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA  | 2562 |
| Db | 2467 | TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA  | 2526 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC--TGCA   | 2619 |
| Db | 2527 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA  | 2586 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAGTTT  | 2679 |
| Db | 2587 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC | 2646 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA  | 2739 |
| Db | 2647 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA  | 2706 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC  | 2799 |
| Db | 2707 | ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC | 2766 |
| Qy | 2800 | AGTGCTAAAGATGATTC--TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC   | 2856 |
| Db | 2767 | AGTTCTAAAGCTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC  | 2826 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG  | 2916 |
| Db | 2827 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGCCTTGACAGAAATTG  | 2886 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA   | 2970 |
| Db | 2887 | CCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAAATCAGTTTCTCA  | 2946 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2971 | GATGAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC  | 3030 |
|    |      |  |      |
| Db | 2947 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT   | 3006 |
| Qy | 3031 | TCTGCTTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA  | 3090 |
|    |      |  |      |
| Db | 3007 | TCTGCTTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA  | 3066 |
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA   | 3150 |
|    |      |  |      |
| Db | 3067 | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA   | 3126 |
| Qy | 3151 | TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG   | 3210 |
|    |      |  |      |
| Db | 3127 | TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG   | 3186 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC  | 3270 |
|    |      |  |      |
| Db | 3187 | AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC  | 3246 |
| Qy | 3271 | ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG   | 3330 |
|    |      |  |      |
| Db | 3247 | ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG   | 3306 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3390 |
|    |      |  |      |
| Db | 3307 | ATATACAAGGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA | 3366 |
| Qy | 3391 | TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT   | 3450 |
|    |      |  |      |
| Db | 3367 | TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT   | 3426 |
| Qy | 3451 | CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA   | 3510 |
|    |      |  |      |
| Db | 3427 | CTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGCCTCTTCTTAGTTGATGATTTA   | 3486 |
| Qy | 3511 | GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT   | 3570 |
|    |      |  |      |
| Db | 3487 | GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT   | 3546 |
| Qy | 3571 | AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT   | 3630 |
|    |      |  |      |
| Db | 3547 | AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT   | 3606 |
| Qy | 3631 | GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT   | 3690 |
|    |      |  |      |
| Db | 3607 | GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT   | 3666 |
| Qy | 3691 | GCCATGGCCAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA            | 3740 |
|    |      |  |      |
| Db | 3667 | GCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA            | 3716 |

RESULT 5

AAA23454

ID AAA23454 standard; cDNA; 4093 BP.

XX  
 AC AAA23454;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE cDNA encoding human secreted protein vb22\_1, SEQ ID NO:63.  
 XX  
 KW Human; secreted protein; cancer; tumour; cardiovascular disorder;  
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
 KW neurodegenerative disease; asthma; contraceptive; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1048..3729  
 FT /\*tag= a  
 FT /product= "Human secreted protein vb22\_1"  
 FT CDS 152..1006  
 FT /\*tag= b  
 FT /product= "Clone vb22\_1 ORF2"  
 XX  
 PN WO200011015-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 24-AUG-1999; 99WO-US19351.  
 XX  
 PR 24-AUG-1998; 98US-0097638.  
 PR 24-AUG-1998; 98US-0097659.  
 PR 09-SEP-1998; 98US-0099618.  
 PR 28-SEP-1998; 98US-0102092.  
 PR 25-NOV-1998; 98US-0109978.  
 PR 23-DEC-1998; 98US-0113645.  
 PR 23-DEC-1998; 98US-0113646.  
 PR 23-AUG-1999; 99US-0379246.  
 XX  
 PA (ALPH-) ALPHAGENE INC.  
 XX  
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
 XX  
 DR WPI; 2000-224657/19.  
 DR P-PSDB; AAY95012, AAY95030.  
 XX  
 PT New secreted or transmembrane proteins and polynucleotides encoding  
 PT them, useful for treating neurodegenerative disorders, autoimmune  
 PT diseases and cancer -  
 XX  
 PS Claim 72; Page 321-322; 357pp; English.  
 XX  
 CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted  
 CC proteins of the invention include those that are thought to be only  
 CC partially secreted, i.e., transmembrane proteins. The proteins of the  
 CC invention may exhibit one or more activities selected from the following:  
 CC cytokine activity; cell proliferation; differentiation; immune  
 CC modulation; haematopoiesis regulation; tissue growth activity;

CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic  
 CC and thrombolytic activity; anti-inflammatory activity; and tumour  
 CC inhibition activity. The proteins may be administered to patients as  
 CC vaccines, and the nucleotides may be used as part of a gene therapy  
 CC regime. Diseases or conditions that may be treated using the proteins or  
 CC nucleotides of the invention include autoimmune diseases; genetic  
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,  
 CC fungal and viral infections, especially HIV; multiple sclerosis;  
 CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;  
 CC insulin dependent diabetes mellitus; and allergic reactions such as  
 CC asthma and anaemia. They may also be used for treating wounds, burns,  
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic  
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may  
 CC additionally be useful as contraceptives. Nucleic acid sequences of the  
 CC invention may be used in chromosome mapping, and as a source of  
 CC diagnostic primers and probes. The present sequence represents cDNA  
 CC encoding one of the 40 proteins of the invention.

XX

SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 other;

Query Match 62.4%; Score 2333.2; DB 21; Length 4093;  
 Best Local Similarity 81.3%; Pred. No. 0;  
 Matches 3017; Conservative 0; Mismatches 573; Indels 120; Gaps 22;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 134 | CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT | 193 |
|    |     |   |     |
| Db | 33  | CTCGGCTCAGTCGGCCAGCCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGCT   | 92  |
| Qy | 194 | CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC  | 252 |
|    |     |   |     |
| Db | 93  | CTGAGACGCGGCCCCGGCGGCGGCGGCGGAGCAGCTGCAGCATCATC-TCCACCTCCAGCC | 151 |
| Qy | 253 | ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT  | 312 |
|    |     |   |     |
| Db | 152 | ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTTCGGACAGCCACCCCGGCCG   | 208 |
| Qy | 313 | CCGCCCCGCTTCAAGTACCAGTTCTGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG | 372 |
|    |     |   |     |
| Db | 209 | CAGCCCGCGTTCAGTACCAGTTCTGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG  | 265 |
| Qy | 373 | GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG  | 432 |
|    |     |   |     |
| Db | 266 | GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG  | 325 |
| Qy | 433 | CCCGCAGCCGGGCTGTCCGAGCTGCGGTGC-----CGCCCGCCCGCCCGCGCCGCTG     | 486 |
|    |     |   |     |
| Db | 326 | CCCGCCCGCGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCGGCGCGCCCTG       | 385 |
| Qy | 487 | CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCGCGGGCCGCTGCCGCGCGCGCCC    | 546 |
|    |     |   |     |
| Db | 386 | ATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCGGGGACCCCTGCCGCGCGCTCCC     | 445 |
| Qy | 547 | CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC      | 597 |
|    |     |   |     |
| Db | 446 | CCCGTCGCCCCGGAGCGGCGGCGGCTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC | 505 |



Qy 598 GCGCCATCCCTGCCGCCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657  
 |||||  
 Db 506 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 565

Qy 658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711  
 |||||  
 Db 566 CCTCCGGCCCCGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 625

Qy 712 -----CCCGCCGCGCCCCCTTCCACGCGCGCGCGCCCAAGCGC 750  
 |||||  
 Db 626 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCGCGCCCAAGCGC 685

Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807  
 |||||  
 Db 686 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 745

Qy 808 GTGATACCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867  
 |||||  
 Db 746 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 802

Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927  
 |||||  
 Db 803 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 862

Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA 987  
 |||||  
 Db 863 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 922

Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047  
 |||||  
 Db 923 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTGAGTGAAGCTTCTAAAGAGGTCTCA 982

Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107  
 |||||  
 Db 983 GAGAAGGCAA-AACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1041

Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167  
 |||||  
 Db 1042 TCAGAAATGGGATCATCGTTGAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1101

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224  
 |||||  
 Db 1102 AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAAGTTAGTTAGTAAT 1161

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269  
 |||||  
 Db 1162 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1221

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA 1329  
 |||||  
 Db 1222 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGA 1281

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
 |||||  
 Db 1282 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACATTTGAGCGAGTATGGGAAGTGAAA 1341

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437

|    |      |  |      |
|----|------|--|------|
| Db | 1342 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG   | 1398 |
| Qy | 1438 | GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG   | 1497 |
| Db | 1399 | GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACCTAATCACGAAAAA  | 1458 |
| Qy | 1498 | GATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC  | 1557 |
| Db | 1459 | GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT   | 1518 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA   | 1614 |
| Db | 1519 | CGTTCAGGAGCATATATCATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA     | 1578 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA     | 1674 |
| Db | 1579 | ACAAACATTTTTCTTTGTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA      | 1638 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAACGTCAAAT    | 1731 |
| Db | 1639 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC   | 1698 |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA   | 1791 |
| Db | 1699 | CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA   | 1758 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCA   | 1851 |
| Db | 1759 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG   | 1818 |
| Qy | 1852 | GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAA    | 1911 |
| Db | 1819 | GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAA    | 1878 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTT   | 1971 |
| Db | 1879 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT   | 1938 |
| Qy | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG   | 2031 |
| Db | 1939 | TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAAGTTTTGCCTGACATTGTTATG  | 1998 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA    | 2091 |
| Db | 1999 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA    | 2058 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC   | 2151 |
| Db | 2059 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAAC    | 2115 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA   | 2208 |
| Db | 2116 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA    | 2175 |
| Qy | 2209 | GGAATAAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA | 2268 |

|    |      |  |      |
|----|------|--|------|
| Db | 2176 | GAAATTAAAGAGCCTGAAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA  | 2235 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC  | 2328 |
|    |      |  |      |
| Db | 2236 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC  | 2295 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG  | 2388 |
|    |      |  |      |
| Db | 2296 | TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCTGATCATTCTGAGCTAGTT   | 2355 |
| Qy | 2389 | GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA  | 2448 |
|    |      |  |      |
| Db | 2356 | GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC   | 2415 |
| Qy | 2449 | GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A     | 2502 |
|    |      |  |      |
| Db | 2416 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA   | 2475 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA   | 2562 |
|    |      |  |      |
| Db | 2476 | TTTGAGTCAATGATAGAAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA  | 2535 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA   | 2619 |
|    |      |  |      |
| Db | 2536 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA   | 2595 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT  | 2679 |
|    |      |  |      |
| Db | 2596 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC  | 2655 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA   | 2739 |
|    |      |  |      |
| Db | 2656 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA   | 2715 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC   | 2799 |
|    |      |  |      |
| Db | 2716 | ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC  | 2775 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC   | 2856 |
|    |      |  |      |
| Db | 2776 | AGTTCTAAACATGATTCAATTTCTAAATTAGCCAGGAATATACTGACCTAGAAGTATCC    | 2835 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG  | 2916 |
|    |      |  |      |
| Db | 2836 | CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACACAGAATTG | 2895 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA    | 2970 |
|    |      |  |      |
| Db | 2896 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA   | 2955 |
| Qy | 2971 | GATGAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC  | 3030 |
|    |      |  |      |
| Db | 2956 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT   | 3015 |
| Qy | 3031 | TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA   | 3090 |
|    |      |  |      |
| Db | 3016 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA   | 3075 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA   | 3150 |
|    |      |  |      |
| Db | 3076 | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA   | 3135 |
| Qy | 3151 | TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG   | 3210 |
|    |      |  |      |
| Db | 3136 | TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG   | 3195 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTACAGC | 3270 |
|    |      |  |      |
| Db | 3196 | AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTCATTGACAGTATTCAGC | 3255 |
| Qy | 3271 | ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG   | 3330 |
|    |      |  |      |
| Db | 3256 | ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG   | 3315 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3390 |
|    |      |  |      |
| Db | 3316 | ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3375 |
| Qy | 3391 | TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT   | 3450 |
|    |      |  |      |
| Db | 3376 | TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT   | 3435 |
| Qy | 3451 | CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA   | 3510 |
|    |      |  |      |
| Db | 3436 | CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA   | 3495 |
| Qy | 3511 | GTTGATTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT     | 3570 |
|    |      |  |      |
| Db | 3496 | GTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT     | 3555 |
| Qy | 3571 | AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT   | 3630 |
|    |      |  |      |
| Db | 3556 | AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT   | 3615 |
| Qy | 3631 | GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT   | 3690 |
|    |      |  |      |
| Db | 3616 | GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAAATGTTAAAGAT  | 3675 |
| Qy | 3691 | GCCATGGCCAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA            | 3740 |
|    |      |  |      |
| Db | 3676 | GCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA            | 3725 |

# RESULT 6

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

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XX
OS Homo sapiens.
XX
PN US6426186-B1.
XX
PD 30-JUL-2002.
XX
PF 18-JAN-2000; 2000US-0484970.
XX
PR 18-JAN-2000; 2000US-0484970.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Volkmuth W, Walker MG;
XX
DR WPI; 2002-673014/72.
XX
PT A combination of polynucleotides which are co-expressed with genes
PT known to be involved in bone remodeling and osteoporosis are useful in
PT an array for the diagnosis of bone remodeling and osteoporosis
PT associated disorders -
XX
PS Claim 1; Column 283-288; 206pp; English.
XX
CC The invention relates to a combination comprising a number of
CC substantially purified and isolated polynucleotides which are
CC co-expressed with genes known to be involved in bone remodelling and
CC osteoporosis. The invention is used to diagnose disorders associated
CC with bone remodelling or osteoporosis. ABS70344-ABS70512 represent
CC human bone remodelling genes of the invention.
XX
SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 15 other;

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Query Match 62.1%; Score 2323.8; DB 24; Length 4822;  
Best Local Similarity 80.9%; Pred. No. 0;  
Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 63  | CGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTGCGCTCTGCAGGTTCTTTCG | 122 |
|    |     |   |     |
| Db | 78  | CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTACCCACAGTAGGTCCCTCG  | 137 |
| Qy | 123 | GCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAAC | 182 |
|    |     |   |     |
| Db | 138 | GCTCAGT-----CGGCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAAC             | 182 |
| Qy | 183 | CGCCCGCGACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG  | 241 |
|    |     |   |     |
| Db | 183 | CGCCCGCGGCTCTGAGACGCGGCCCCGNGGCGGCGGCAGCAGCTGCAGCATCATC-TCC   | 241 |
| Qy | 242 | ACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCC  | 301 |
|    |     |   |     |
| Db | 242 | ACCCTCCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCTGGACAGCC  | 298 |
| Qy | 302 | CGCCCCGGCCTCCGCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCAGGACGAGGAGG   | 361 |
|    |     |   |     |
| Db | 299 | CACCCCGGCCCGCAGCCCGGTTCAAGTACCAGTTTCGTGAGGGAGCCCAGGACGAGGAG-  | 357 |

|    |      |   |      |
|----|------|---|------|
| Qy | 362  | ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTGC | 421  |
| Db | 358  | --GAAGAAGAGGANGATGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGC  | 415  |
| Qy | 422  | TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCGCCG    | 475  |
| Db | 416  | TGGAGAGGAAGCCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCG     | 475  |
| Qy | 476  | CCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCGCGGGCCGCTGC    | 535  |
| Db | 476  | GCGCGCCNNTAATGGACTTCGGAATGACTTCGTGCCGCGCGCCCGGGGACCCCTGC      | 535  |
| Qy | 536  | CGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGAGCCCCG-----    | 589  |
| Db | 536  | CGGCCGCTCCCCCGTCGCCCCGAGCGGCAGCCGTCCTGGGACCCGAGCCCGGTGTCGT    | 595  |
| Qy | 590  | ---CGGCGCCCGCGCCATCCCTGCCGCGCGCTGCCGCAGTCCTGCCCTCCAAGCTCCAG   | 646  |
| Db | 596  | CGACCGTGCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTG  | 655  |
| Qy | 647  | AGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGG   | 706  |
| Db | 656  | AGGACGACGAGCCTCCGGCCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGG | 715  |
| Qy | 707  | CGGAGC-----CCGCCGCGCCCCCTTCCACGCCGGCCG                        | 739  |
| Db | 716  | CAGAGCCCGTGTGGANCCCGCCAGCCCCGGCTNCCGCCGCGCCCCCTCCACCCGCGCCG   | 775  |
| Qy | 740  | CGCCCAAGCGCAGGGGCTCC--GGCTCAGTGGATGAGACCCTTTTGTCTTCTCTGCTG    | 796  |
| Db | 776  | CGCCCAAGCGCAGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTTCTCTGCTG   | 835  |
| Qy | 797  | CATCTGAGCCTGTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAG   | 856  |
| Db | 836  | CATCTGAGCCTGTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAG   | 892  |
| Qy | 857  | GTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTCTGCTTGAACTGCTGCCT  | 916  |
| Db | 893  | GTAACACTATTTCGGCTGGTCAAGAGGATTTCCCATCTGTCTCTGCTTGAACTGCTGCTT  | 952  |
| Qy | 917  | CTCTTCCCTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTA  | 976  |
| Db | 953  | CTCTTCCCTCTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTA  | 1012 |
| Qy | 977  | ACTTATCAGCAGTGTCACTCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTA  | 1036 |
| Db | 1013 | ATTTGTCAACAGTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTA  | 1072 |
| Qy | 1037 | AAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAAATTTTCAG | 1096 |
| Db | 1073 | AAGAGGTCTCAGAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAG | 1132 |
| Qy | 1097 | AATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCA  | 1156 |
| Db | 1133 | AATTAGAATACTCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAACTGCGCG  | 1192 |
| Qy | 1157 | TATTAGTAGAAAAACATAAGGAAGAAGTAATTGTGAGGAGTAAA--GACAAAGAGGATT   | 1213 |

|    |      |   |      |
|----|------|---|------|
| Db | 1193 | TAATAGTAGCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGT  | 1252 |
| Qy | 1214 | TAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGG            | 1258 |
| Db | 1253 | TAGTTAGTAATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGG  | 1312 |
| Qy | 1259 | GTAAAGAAGACAGAGTTGTGTCTCCAGAAAAACAATGGACATTTTAAATGAAATGCAGA   | 1318 |
| Db | 1313 | TTAAAGAGGATGAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAGAGAG   | 1372 |
| Qy | 1319 | TGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCAT  | 1378 |
| Db | 1373 | TTGCAGTGGAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTAT  | 1432 |
| Qy | 1379 | GGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----    | 1431 |
| Db | 1433 | GGGAAGTGAAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCG   | 1489 |
| Qy | 1432 | -----AATGTGGAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAA   | 1486 |
| Db | 1490 | AGAGCAACTTGGAAGTAAAGTGATAAAAAATGTTTGCAGATAGCCTTGAGCAAATA      | 1549 |
| Qy | 1487 | GTCTTGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAAC   | 1546 |
| Db | 1550 | ATCACGAAAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAG  | 1609 |
| Qy | 1547 | CTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCG  | 1603 |
| Db | 1610 | GTATAAAGGATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTG  | 1669 |
| Qy | 1604 | AAAGCACACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAG   | 1663 |
| Db | 1670 | AGAGCATTGCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCG  | 1729 |
| Qy | 1664 | ATG-AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCC  | 1719 |
| Db | 1730 | ATGAAAAAAAAAATAGAAGAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACC   | 1789 |
| Qy | 1720 | AAAACGTCAAATCC-TTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAAC  | 1778 |
| Db | 1790 | AAAACATCAAACCCTTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC  | 1849 |
| Qy | 1779 | AGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAATGCCTGAAGGTCTGACGCC   | 1838 |
| Db | 1850 | AGATAATTTAACAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC   | 1909 |
| Qy | 1839 | AGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGC | 1898 |
| Db | 1910 | AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC  | 1969 |
| Qy | 1899 | TTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCC  | 1958 |
| Db | 1970 | TTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC   | 2029 |
| Qy | 1959 | CACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGGCC  | 2018 |

|    |      |  |      |
|----|------|--|------|
| Db | 2030 | TGCAGCACAGCTTTGCCCATCATTTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC  | 2089 |
| Qy | 2019 | TGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGT   | 2078 |
| Db | 2090 | TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCTAGTGCTGGTGCTTCCGTGAT    | 2149 |
| Qy | 2079 | GCAGCCCAGTGATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCT    | 2138 |
| Db | 2150 | ACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACA   | 2206 |
| Qy | 2139 | TGAGCCTGAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTT    | 2195 |
| Db | 2207 | TGAGCCTGAAAACCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC     | 2266 |
| Qy | 2196 | GGGAACAAAGGAAGGAATAAAAGAGCCTGAAAAGTTTAAATGCAGCTGTTTCAGGAAACAGA | 2255 |
| Db | 2267 | AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA   | 2326 |
| Qy | 2256 | AGCTCCTTATATATCCATTGCGTGTGATTAAATTAAAGAAACAAAGCTCTCCACTGAGCC   | 2315 |
| Db | 2327 | AGCTCCTTATATATCTATTGCATGTGATTAAATTAAAGAAACAAAGCTTCTGCTGAACC    | 2386 |
| Qy | 2316 | AAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACA   | 2375 |
| Db | 2387 | AGCTCCGGATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCA   | 2446 |
| Qy | 2376 | CGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGA  | 2435 |
| Db | 2447 | TTCTGAGCTAGTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA  | 2506 |
| Qy | 2436 | TTCGATTCTCGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCT   | 2495 |
| Db | 2507 | TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT   | 2566 |
| Qy | 2496 | CACTGA-----AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCCTC   | 2549 |
| Db | 2567 | CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTT   | 2626 |
| Qy | 2550 | ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAA   | 2609 |
| Db | 2627 | GCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAA   | 2686 |
| Qy | 2610 | AGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCA   | 2666 |
| Db | 2687 | AGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCA   | 2746 |
| Qy | 2667 | AATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTCTAAGGAAGA    | 2726 |
| Db | 2747 | GATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTCTAAGGAAGC    | 2806 |
| Qy | 2727 | CAAAATAAAAGAAAGTGAAACATTTTCAGATTCTCCGATTGAGATAATAGATGAATT      | 2786 |
| Db | 2807 | ACAGATAAGAGAAACTGAAACGTTTTCAGATTCTCCAATTGAAATATAGATGAGTT       | 2866 |
| Qy | 2787 | TCCCACGTTTGTGAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGA   | 2843 |
| Db | 2867 | CCCTACATTGATCAGTTCTAAAACCTGATTCAATTTCTAAATTAGCCAGGGAATATACTGA  | 2926 |



|    |      |   |      |
|----|------|---|------|
| Qy | 2844 | TCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCC   | 2903 |
|    |      |   |      |
| Db | 2927 | CCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCC     | 2986 |
| Qy | 2904 | TTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCC'TAAAGATGAAG----   | 2959 |
|    |      |   |      |
| Db | 2987 | TTGCACAGAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAA     | 3046 |
| Qy | 2960 | --TACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATC    | 3017 |
|    |      |   |      |
| Db | 3047 | AATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATT    | 3106 |
| Qy | 3018 | GCCTTCAAATGTCTCTGCTTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAA    | 3077 |
|    |      |   |      |
| Db | 3107 | GCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAA    | 3166 |
| Qy | 3078 | ATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATC    | 3137 |
|    |      |   |      |
| Db | 3167 | AGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATC    | 3226 |
| Qy | 3138 | CCTGTCAGCTGTATTGTCAGCAGAGCTGAG-TAAAACTTCAGTTGTTGACCTCCTCTACT    | 3196 |
|    |      |   |      |
| Db | 3227 | ACCATCTGCTATATTTTCAGCAGAGCTGAGCTAAAACTTCAGTTGTTGACCTCCTGTACT    | 3286 |
| Qy | 3197 | GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC   | 3256 |
|    |      |   |      |
| Db | 3287 | GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCAT   | 3346 |
| Qy | 3257 | TGACAGTGTTTCAGCATTTGTTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA | 3316 |
|    |      |   |      |
| Db | 3347 | TGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA   | 3406 |
| Qy | 3317 | CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC    | 3376 |
|    |      |   |      |
| Db | 3407 | CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC    | 3466 |
| Qy | 3377 | ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAAT  | 3436 |
|    |      |   |      |
| Db | 3467 | ACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAT  | 3526 |
| Qy | 3437 | ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT     | 3496 |
|    |      |   |      |
| Db | 3527 | ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT     | 3586 |
| Qy | 3497 | TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATG      | 3556 |
|    |      |   |      |
| Db | 3587 | TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATG      | 3646 |
| Qy | 3557 | TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA    | 3616 |
|    |      |   |      |
| Db | 3647 | TGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG    | 3706 |
| Qy | 3617 | TTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA     | 3676 |
|    |      |   |      |
| Db | 3707 | TTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA     | 3766 |

[illegible]

## RESULT 7

ABX34563

ID ABX34563 standard; cDNA; 4698 BP.

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AC ABX34563:

XX

DT 13-FEB-2003 (first entry)

XX

DE Human mddt cDNA SEO ID 124.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;  
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
KW gene therapy; protein replacement therapy; cell proliferative disorder;  
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
KW psoriasis; hepatitis; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX

PD 10-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US09944.

XX

PR 28-MAR-2001; 2001US-279619P.

PR 29-MAR-2001: 2001US-280067P.

PR 29-MAR-2001; 2001US-280068P.

PR 16-MAY-2001; 2001US-291280P.

PR 17-MAY-2001; 2001US-291829P.

PR 17-MAY-2001; 2001US-291849P.

PR 19-JUN-2001; 2001US-299428P.

PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-058431/05.

DR P-PSDB; ABU11573.

XX



Df  
376 TGGACTTTCGGAATGACTTCGTGCCCGCCGCCTCCCGGGACCCCCTGCCGCGCCTTTCCC 435

Qy  
548 CTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCCG 598  
| | ||||| || ||||| ||||||| | ||||||| | ||||| |  
Df  
436 CCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCCGTGTCTGTCGACCCTGCCCG 495

Qy  
599 CGCCATCCCCTGCCGCCCCGTGCCGCAGTCTTGCCCTCCAAGCTCCCAGAGGACGACGAGC 658  
||||||| || | ||||||| ||||| ||||||| ||||||| ||||||| |||||||  
Df  
496 CGCCATCCCCGCTGTCTGTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGC 555

Qy  
659 CTCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711  
||||||| ||||| ||||| || ||||| || ||||| ||||| ||||| |||||  
Df  
556 CTCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGT 615

Qy  
712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGCA 751  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Df  
616 GGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGCA 675

Qy  
752 GGGGCTCC----GGCTCAGTGGAATGAGACCC--TTTTTGCTCTTCTGCTGCATCTGAGC 805  
||||||| | ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Df  
676 GGGGCTCCTCGGGCTCAGATGGATGAGACCATTTTTTGCTCTTACCTGCTGCATCTGAGC 735

Qy  
806 CTGTGATA CCTCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACTG 865  
||||||| ||||| | | || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Df  
736 CTGTGATACGCTCCTC--ATGCAGAAAATATGGACTTGAAGGAGCAGCCAGGTAACTA 793

Qy  
866 TTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGA AACTGCTGCCTCTCTTCCTT 925  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Df  
794 TTTCGGCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGA AACTGCTGCCTCTCTTCCTT 853

Qy  
926 CTCTATCTCCTCTCTCAACTGTTTCTTTTAAGAACAATGGATACCTTGGTAACCTTATCAG 985  
||| ||||||| ||||| | ||||| ||||||| ||||||| ||||||| ||||| |||||  
Df  
854 CTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACAATGAATACCTTGGTAATTTGTCAA 913

Qy  
986 CAGTGTCATCCTCAGAAGGAACAATTGAAG- AAACTTTAAATGAAGCTTCTAAAGAGTTG 1044  
|||| | || ||||||| || ||||| || ||||| || ||||| ||||||| ||||||| |||||  
Df  
914 CAGTATTACCACTGAAGGAACACTTCAAGAAAAATGTGAGTGAAGCTTCTAAAGAGGTC 973

Qy  
1045 CCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAA 1104  
||||||| ||||| || || || ||||| ||||||| ||||| ||||||| ||||||| |||||||  
Df  
974 TCAGAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAA 1033

Qy  
1105 TATTTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTA 1164  
|| ||||||| ||||||| || | ||||| ||||||| ||||| ||||| ||||| ||||| |||||  
Df  
1034 TACTTCAGAAATGGGATCATCGTTGAGTGTCTTCCAAAAGCAGAATCTGCCGTAATAGTA 1093

Qy  
1165 GAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGT 1221  
| ||| ||| ||||||| ||||| ||||| | ||||| || ||||||| ||||||| |||||  
Df  
1094 GCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGT 1153

Qy  
1222 AGTGCAGCCCTTACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA 1266  
| | ||||| | || ||||||| ||||| ||||||| ||||||| ||||||| |||||||  
Df  
1154 AATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAG 1213

Qy  
1267 GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTGAGTA 1326  
|| ||||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| |||||  
Df  
1214 GATGAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAAGT 1273

|    |      |   |      |
|----|------|---|------|
| Qy | 1327 | GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTTGAACAAGCATGGGAAGTG | 1386 |
| Db | 1274 | GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG  | 1333 |
| Qy | 1387 | AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AAT         | 1434 |
| Db | 1334 | AAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAGGCGAGAGCAAGG | 1405 |
| Qy | 1435 | GTGGAAGTAAAGTGGACAGAAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGGG | 1494 |
| Db | 1391 | TTGGAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAA   | 1450 |
| Qy | 1495 | AAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAG   | 1554 |
| Db | 1451 | AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG  | 1510 |
| Qy | 1555 | GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACC  | 1611 |
| Db | 1511 | GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT  | 1570 |
| Qy | 1612 | ACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA  | 1671 |
| Db | 1571 | GCAACAAACATTTTTCCTTTGTTAGGAGATCTACTTCAGAAAATAAGACCGATGAAAAA   | 1630 |
| Qy | 1672 | AAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCA  | 1728 |
| Db | 1631 | AAAATAGAAGAAAAGAAGGCCCAAATAGTAAACAGAGAAGAATACTAGCACCAAAACATCA | 1690 |
| Qy | 1729 | AATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTA  | 1788 |
| Db | 1691 | AACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA    | 1750 |
| Qy | 1789 | TCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTT  | 1848 |
| Db | 1751 | ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA  | 1810 |
| Qy | 1849 | CAGGAAGCATGTGAAAGTGAATGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACA   | 1908 |
| Db | 1811 | CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA  | 1870 |
| Qy | 1909 | AAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAG   | 1968 |
| Db | 1871 | AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG  | 1930 |
| Qy | 1969 | CTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTT  | 2028 |
| Db | 1931 | CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT  | 1990 |
| Qy | 2029 | ATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGT   | 2088 |
| Db | 1991 | ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGC   | 2050 |
| Qy | 2089 | GTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAA  | 2148 |
| Db | 2051 | TCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA  | 2107 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2149 | AACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT--AAAAGCTTTGGGAACAAAG   | 2205 |
| Db | 2108 | AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG   | 2167 |
| Qy | 2206 | GAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTAT | 2265 |
| Db | 2168 | GAAGAAATTTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT | 2227 |
| Qy | 2266 | ATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAT  | 2325 |
| Db | 2228 | ATATCTATTGTCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGTCCGGAT  | 2287 |
| Qy | 2326 | TTCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTA | 2385 |
| Db | 2288 | ATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAAAGAT      | 2347 |
| Qy | 2386 | GTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCTT | 2445 |
| Db | 2348 | GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT | 2407 |
| Qy | 2446 | GAAGTCCCACAAACACAAAGAGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA----  | 2501 |
| Db | 2408 | GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT  | 2467 |
| Qy | 2502 | --AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAG  | 2559 |
| Db | 2468 | TCATTTGAGTCAATGATAGAAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAG | 2527 |
| Qy | 2560 | CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T  | 2616 |
| Db | 2528 | GGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTTG  | 2587 |
| Qy | 2617 | GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAG  | 2676 |
| Db | 2588 | TTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAG | 2647 |
| Qy | 2677 | TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA  | 2736 |
| Db | 2648 | CTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGA  | 2707 |
| Qy | 2737 | GAAAGTGAAACATTTTCAGATTGATCTCCGATTGAGATAATAGATGAATTTCCACGTTT   | 2796 |
| Db | 2708 | GAAACTGAAACGTTTTCAGATTGATCTCCAATTGAAATTATAGATGAGTTCCCTACATTG  | 2767 |
| Qy | 2797 | GTCAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA  | 2853 |
| Db | 2768 | ATCAGTTCTAAAAGTATTGATTTCTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTA | 2827 |
| Qy | 2854 | TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTGATTCGCTTGTCTAGAA  | 2913 |
| Db | 2828 | TCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTGATTCGCTTGCACAGAA   | 2887 |
| Qy | 2914 | TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTT   | 2967 |
| Db | 2888 | TTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTC   | 2947 |
| Qy | 2968 | TCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAAT  | 3027 |

|    |         |   |      |
|----|---------|---|------|
| Db | 2948    | TCAGATGACTTTTCTAAAAATGGGTCCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGAT   | 3007 |
| Qy | 3028    | GTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACG    | 3087 |
| Db | 3008    | GTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTG    | 3067 |
| Qy | 3088    | AAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCT    | 3147 |
| Db | 3068    | AAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCT    | 3127 |
| Qy | 3148    | GTATTGTCAGCAGAGCTGAGTAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGACATT     | 3207 |
| Db | 3128    | ATATTTTCAGCAGAGCTGAGTAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGACATT     | 3187 |
| Qy | ENGTH20 | GACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTC        | 3267 |
| Db | 3188    | AAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATTC   | 3247 |
| Qy | 3268    | AGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTT   | 3327 |
| Db | 3248    | AGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT    | 3307 |
| Qy | 3328    | AGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGG    | 3387 |
| Db | 3308    | AGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGG    | 3367 |
| Qy | 3388    | GCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCT   | 3447 |
| Db | 3368    | GCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAGTACA  ATTCT   | 3427 |
| Qy | 3448    | GCTCTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGAT   | 3507 |
| Db | 3428    | GCTCTTGGTCATGTGAACAGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGAT    | 3487 |
| Qy | 3508    | TTAGTTGATTCCCTGAAGTTTGCACTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTG    | 3567 |
| Db | 3488    | TTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTG    | 3547 |
| Qy | 3568    | TTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCTGTTATT     | 3627 |
| Db | 3548    | TTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATT    | 3607 |
| Qy | 3628    | TATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTAAAG    | 3687 |
| Db | 3608    | TATGAACGGCATCAGGCACAGAT3Y 50XC CTAGGACTTGCAAATAAGAATGTTTAA 2467 | 2467 |
| Qy | 3688    | GATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA           | 3740 |
| Db | 3668    | GATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA           | 3720 |

RESULT 8

AAZ56886.

ID AAZ56886 standard; DNA; 3579 BP.

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AC AAZ56886;





| Accession | Position | Sequence  | Position |
|-----------|----------|---|----------|
| Db        | 1        | ATGGAAGACCTGGACCACTCTCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG    | 57       |
| Qy        | 313      | CCGCCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCAGGACGAGGAGGACGAGGAGGAG  | 372      |
| Db        | 58       | CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCAGGACGAGGAG---GAAGAAGAG   | 114      |
| Qy        | 373      | GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG  | 432      |
| Db        | 115      | GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG  | 174      |
| Qy        | 433      | CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCCGCCGCGCCGCTG  | 486      |
| Db        | 175      | CCCGCCCGCCGGGCTGTCCGCGGCCCACTGCCACCGCCCTGCGCCGCGCGCCCTG       | 234      |
| Qy        | 487      | CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC   | 546      |
| Db        | 235      | ATGGACTTCGGAATGACTTCGTGCCGCCGCGCCCCGGGGACCCCTGCCGGCCGCTCCC    | 294      |
| Qy        | 547      | CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC      | 597      |
| Db        | 295      | CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCTGCCC   | 354      |
| Qy        | 598      | GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCAGAGGACGACGAG    | 657      |
| Db        | 355      | GCGCCATCCCCGTGTCTGTCTGCCGCAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG   | 414      |
| Qy        | 658      | CCTCCGGCGAGGCCCGCCCTCCGCCGCCAGCCGCGCGAGCCCCCTGGCGGAG-----     | 711      |
| Db        | 415      | CCTCCGGCCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG | 474      |
| Qy        | 712      | -----CCCGCCGCGCCCCCTTCCACGCCGGCA CAAGCGC                      | 760      |
| Db        | 475      | TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC   | 534      |
| Qy        | 751      | AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTCTTCTGCTGCATCTGAGCCT   | 807      |
| Db        | 535      | AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTCTTCTGCTGCATCTGAGCCT   | 594      |
| Qy        | 808      | GTGATACCCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT   | 867      |
| Db        | 595      | GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT   | 651      |
| Qy        | 868      | TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT   | 927      |
| Db        | 652      | TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT   | 711      |
| Qy00X9    | 928      | CTATCTCCTCTCTCAACTGTTT CATGGATACCTTGGTAACCTTACACTT            | 9820     |
| Db        | 712      | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA  | 771      |
| Qy        | 988      | GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA   | 1047     |
| Db        | 772      | GTATTACCCACTGAAGGAACAATTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA  | 831      |
| Qy        | 1048     | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT  | 1107     |
| Db        | 832      | GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAAACAGAGTTTTCAGAATTAGAATAC | 891      |

|    |      |   |      |
|----|------|---|------|
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCAAAGGAGAGTCAGCCATATTAGTAGAA    | 1167 |
|    |      |   |      |
| Db | 892  | TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA | 951  |
| Qy | 1168 | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT  | 1224 |
|    |      |   |      |
| Db | 952  | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT  | 1011 |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC            | 1269 |
|    |      |   |      |
| Db | 1012 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT  | 1071 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA  | 1329 |
|    |      |   |      |
| Db |      | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA   | 2280 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA  | 1389 |
|    |      |   |      |
| Db | 1132 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA  | 1191 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG         | 1437 |
|    |      |   |      |
| Db | 1192 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG  | 1248 |
| Qy | 1438 | GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG    | 1497 |
|    |      |   |      |
| Db | 1249 | GAAAGTAAAGTGGATAAAAAATGTTTTCAGATAGCCTTGAGCAAATAATCACGAAAAA    | 1308 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGAC    | 1557 |
|    |      |   |      |
| Db | 1309 | GATAGTGAGAGTAGTAATGATGATACCTTCTTTCCCAGTACGCCAGAAGGTATAAAGGAT  | 1368 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA  | 1614 |
|    |      |   |      |
| Db | 1369 | CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA  | 1428 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA   | 1674 |
|    |      |   |      |
| Db | 1429 | ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA   | 1488 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAACGTCAAAT   | 1731 |
|    |      |   |      |
| Db | 1489 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC  | 1548 |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA  | 1791 |
|    |      | A   |      |
| Db | 1549 | CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTAACA    | 1608 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG  | 1851 |
|    |      |   |      |
| Db | 1609 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG  | 1668 |
| Qy | 1852 | GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA  | 1911 |
|    |      |   |      |
| Db | 1669 | GAAGCATGTGAAAGTGAACTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA  | 1728 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT    | 1971 |
| Db | 1729 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT   | 1788 |
| Qy | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG   | 2031 |
| Db | 1789 | TGCCCATCATTTGAAGAGTCAAGAGCTACTCCTTACCAGTTTTGCCTGACATTGTTATG    | 1848 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA   | 2091 |
| Db | 1849 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA   | 1908 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC   | 2151 |
| Db | 1909 | TC00XA AAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAAG       | 1968 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA   | 2208 |
| Db | 1966 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA    | 2025 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTTCAGGAAACAGAAGCTCCTTATATA | 2268 |
| Db | 2026 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA   | 2085 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT   | 2328 |
| Db | 2086 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTT    | 2145 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG  | 2388 |
| Db | 2146 | TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT  | 2205 |
| Qy | 2389 | GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA   | 2448 |
| Db | 2206 | GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC   | 2265 |
| Qy | 2449 | GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A    | 2502 |
| Db | 2266 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA   | 2325 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA   | 2562 |
| Db | 2326 | TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA   | 2385 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA   | 2619 |
| Db | 2386 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA    | 2445 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAGTTT   | 2679 |
| Db | 2446 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC  | 2505 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA   | 2739 |
| Db | 2506 | AGTACTGCAGTTTATTCAAATGAAAGTCTTATTTCTAAGGAAGCAATAGATAAGAGAA     | 2565 |
| Qy | 2740 | AGTGAACCATTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC     | 2799 |

|    |      |  |      |
|----|------|--|------|
| Db | 2566 | ACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTTACATTGATC            | 2625 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC             | 2856 |
| Db | 2626 | AGTTCTAAAACGTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC            | 2685 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG             | 2916 |
| Db | 2686 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCAAGAATTG               | 2745 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA              | 2970 |
| Db | 2746 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA             | 2805 |
| Qy | DN1  | GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC             | 3030 |
| Db | 2806 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT             | 2865 |
| Qy | 3031 | TCTGCTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA              | 3090 |
| Db | 2866 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA             | 2925 |
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA             | 3150 |
| Db | 2926 | GAAGCTGAGAAAAAACTTCCTTCCGATAAGAGAAAGAGGACAGATCACCATCTGCTATA              | 2985 |
| Qy | 3151 | TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG             | 3210 |
| Db | 2986 | TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCTGCTACTGGA                        | 3045 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC            | 3270 |
| Db | 3046 | AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATTCAGC            | 3105 |
| Qy | 3271 | ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG             | 3330 |
| Db | 3106 | ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG             | 3165 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA            | 3390 |
| Db | 3166 | ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA            | 3225 |
| Qy | 3391 | TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAAGAAATACAGTAATTCTGCT           | 3450 |
| Db | 3226 | TATCTGGAATCTGAAGTTGCT* <del>TAATCTGAG</del> AGTTGGTTTCAAGTACAGTAATTCTGCT | 3285 |
| Qy | 3451 | CTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA            | 3510 |
| Db | 3286 | CTTGGTCATGTGAAGTGCACGATAAAGGAACCTCAGGCGCCTCTTCTTAGTTGATGATTTA            | 3345 |
| Qy | 3511 | GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT              | 3570 |
| Db | 3346 | GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT              | 3405 |
| Qy | 3571 | AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT             | 3630 |

Db 3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTGTATTATTTAT 3465

Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690  
 |||||

Db 3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525  
 |||||

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
 |||||

Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 9

AAF90324

ID AAF90324 standard; cDNA; 3579 BP.

XX

AC AAF90324;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A cDNA.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury;  
 KW brain injury; stroke; neuronal degeneration; Alzheimer's disease;  
 KW Parkinson's disease; neuromuscular disorder; psychiatric disorder; T  
 KW developmental disorder; neuroprotective; nootropic; neuroleptic;  
 KW antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;  
 KW therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB04345.

XX

PR 15-NOV-1999; 99GB-0026995.

PR 24-JAN-2000; 2000GB-0001550.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR P-PSDB; AAB82349.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases -

XX

PS Disclosure; Page 25-26; 25pp; English.

XX

CC The present sequence is that of cDNA encoding human NOGO-A (see  
 CC AAB82349). NOGO-A is a previously known splice variant G 1167  
 CC human NOGO gene on chromosome 2p21. NOGO-A cDNA was obtained by  
 CC PCR amplification of human spinal cord cDNA. The invention  
 CC relates to a novel splice variant, NOGO-C (see AAF90323). It

provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels.

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 61.2%; Score 2289.2; DB 22; Length 3579;  
 Similarity 81.5%; Pred. ~~NCACAGA~~7 -75XT  
 Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

[illegible]

|    |      |   |      |
|----|------|---|------|
| Qy | 808  | GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACTGTT    | 867  |
|    |      |   |      |
| Db | 595  | GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACTATT     | 651  |
| Qy | 868  | TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT   | 927  |
|    |      |   |      |
| Db | 652  | TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT   | 711  |
| Qy | 928  | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA  | 987  |
|    |      |   |      |
| Db | 712  | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA  | 771  |
| Qy | 988  | GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA   | 1047 |
|    |      |   |      |
| Db | 772  | GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA  | 831  |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT  | 1107 |
|    |      |   |      |
| Db | 832  | GAGAAGGCAAAAATCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC   | 891  |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA  | 1167 |
|    |      |   |      |
| Db | 892  | TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA  | 951  |
| Qy | 1168 | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA--GACAAAGAGGATTTAGTTTGTAGT   | 1224 |
|    |      |   |      |
| Db | 952  | AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT   | 1011 |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC            | 1269 |
|    |      |   |      |
| Db | 1012 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT  | 1071 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA  | 1329 |
|    |      |   |      |
| Db | 1072 | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA   | 1131 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA  | 1389 |
|    |      |   |      |
| Db | 1132 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACATTTGAGCGAGTATGGGAAGTGAAA   | 1191 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG         | 1437 |
|    |      |   |      |
| Db | 1192 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAAATCGAGAGCAACTTG | 1248 |
| Qy | 1438 | GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG   | 1497 |
|    |      |   |      |
| Db | 1249 | GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA   | 1308 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC   | 1557 |
|    |      |   |      |
| Db | 1309 | GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT  | 1368 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA  | 1614 |
|    |      |   |      |
| Db | 1369 | CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA  | 1428 |

|     |      |   |                 |
|-----|------|---|-----------------|
| Qy  | 1615 | GCAAACACTTTTCCCTTTGTAGAGAATCATACTTCAGAAAATAAAACAGATGAAAAAAAA      | 1674            |
|     |      |   |                 |
| Db  | 1429 | ACAAACATTTTTCCTTTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA       | 1488            |
| Qy  | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG--ACTAGCCCCAAAACGTCAAAT       | 1731            |
|     |      |   |                 |
| Db  | 1489 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC       | 1548            |
| Qy  | 1732 | CCTTTTCCTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA      | 1791            |
|     |      |   |                 |
| Db  | 1549 | CCTTTTCCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTAACA        | 1608            |
| Qy  | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG      | 1851            |
|     |      |   |                 |
| Db  | 160  |   |                 |
| Qy  | 1852 | GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA      | 1911            |
|     |      |   |                 |
| Db  | 1669 | GAAGCATGTGAAAGTGAACTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA      | 1728            |
| Qy  | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT       | 1971            |
|     |      |   |                 |
| Db  | 1729 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT      | 1788            |
| Qy  | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG      | 2031            |
|     |      |   |                 |
| Db  | 1789 | TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTGCCTGACATTGTTATG       | 1848            |
| Qy  | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA      | 2091            |
|     |      |   |                 |
| Db  | 1849 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA      | 1908            |
| Qy  | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC      | 2151            |
|     |      |   |                 |
| Db  | 1909 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAAATGAGCCTGAAAAC       | 1965            |
| Qy  | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA      | 2208            |
|     |      |   |                 |
| Db  | 1966 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA       | 2025            |
| Qy  | 2209 | GGAATAAAAGAGCCTGAAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA    | 2268            |
|     |      |   |                 |
| Db  | 2026 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAAAGAAGCTCCTTATATA       | 2085            |
| Qy  | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC      | 2328            |
|     |      |   |                 |
| Db  | 2086 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTC      | 2145            |
| Qy  | 2329 | TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG      | 2388            |
|     |      |   |                 |
| Db  | 2146 | TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT      | 2205            |
| Qy  | 2389 | GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCTTGAA     | 2448            |
|     |      |   |                 |
| Db  | 2206 | GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC      | 2265            |
| QyX | 2449 | <del>GAGGTGATATGGAAGTGGAGGCATGATGCTTGAAGGAGAGTCTGATGATGACAT</del> | <del>2568</del> |



|    |      |   |      |
|----|------|---|------|
| Db | 2266 | <div>     </div> GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA   | 2325 |
| Qy | 2503 | <div>   </div> GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA     | 2562 |
| Db | 2326 | <div>     </div> TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA   | 2385 |
| Qy | 2563 | <div>     </div> GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA   | 2619 |
| Db | 2386 | <div>     </div> GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA   | 2445 |
| Qy | 2620 | <div>     </div> TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT  | 2679 |
| Db | 2446 | <div>     </div> CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC  | 2505 |
| Qy | 2680 | <div>     </div> AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA   | 2739 |
| Db | 2506 | <div>     </div> AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA   | 2565 |
| Qy | 2740 | <div>     </div> AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC  | 2799 |
| Db | 2566 | <div>     </div> ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTTACATTGATC  | 2625 |
| Qy | 2800 | <div>     </div> AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC   | 2856 |
| Db | 2626 | <div>     </div> AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC   | 2685 |
| Qy | 2857 | <div>     </div> GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG  | 2916 |
| Db | 2686 | <div>     </div> CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTG  | 2745 |
| Qy | 2917 | <div>     </div> CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA    | 2970 |
| Db | 2746 | <div>     </div> CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA   | 2805 |
| Qy | 2971 | <div>     </div> GATGAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC  | 3030 |
| Db | 2806 | <div>     </div> GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCCTCCAGATGTT  | 2865 |
| Qy | 3031 | <div>     </div> TCTGCTTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA   | 3090 |
| Db | 2866 | <div>     </div> TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA   | 2925 |
| Qy | 3091 | <div>     </div> GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA   | 3150 |
| Db | 2926 | <div>     </div> GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA   | 2985 |
| Qy | 3151 | <div>     </div> TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG   | 3210 |
| Db | 2986 | <div>     </div> TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG   | 3045 |
| Qy | 3211 | <div>     </div> AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC | 3270 |
| Db | 3046 | <div>     </div> AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC  | 3105 |
| Qy | 3271 | <div>     </div> ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG   | 3330 |

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Db      3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165
Qy      3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA 3390
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA 3225
Qy      3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT 3450
        ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCT 3285
Qy      3451 CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345
Qy      3511 GTTGATTCCCTGAAGTTTGCACTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTTC 3570
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3346 GTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405
Qy      3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTTATTTAT 3465
Qy      3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525
Qy      3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

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# RESULT 10

ABN86601

ID ABN86601 standard; DNA; 3579 BP.

XX

AC ABN86601;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo encoding DNA.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
KW neurotransmitter receptor; human; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3579

FT /\*tag= a

FT /product= "Nogo"

FT /note= "Nogo-A, Nogo-B and Nogo-C"

XX

PN US2002072493-A1.

XX  
 PD 13-JUN-2002.  
 XX  
 PF 28-JUN-2001; 2001US-0893348.  
 XX  
 PR 19-MAY-1998; 98IL-0124500.  
 PR 21-JUL-1998; 98WO-US14715.  
 PR 22-DEC-1998; 98US-0218277.  
 PR 19-MAY-1999; 99US-0314161.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR P-PSDB; ABB81078, ABB81079, ABB81080.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in  
 PT the central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides -  
 XX  
 PS Disclosure; Page 49-53; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease  
 CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents a DNA  
 CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B  
 CC and Nogo-C), an example of NS-specific antigen.  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 61.2%; Score 2289.2; DB 24; Length 3579;  
Best Local Similarity 81.5%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCT 312
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCTGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      58 CAGCCCGCGTTCAAGTACCAGTTCTGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      115 GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGG GGTGCTGGAGAGGAAG 174

Qy      433 CCCGCGCCGGGCTGTCCGCGCTGCGGTGC-----CGCCCGCCCGCCCGCGCCGCTG 486
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      175 CCCGCGCCGGGCTGTCCGCGGCCCGAGTGCCACCGCCCTGCGCGCGCGCCCGCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCGCGGGCCGCTGCCGCGCGCGCCC 546
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      235 ATGGACTTCGGAATGACTTCGTGCCGCGCGCCCGGGGACCCCTGCCGCGCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      295 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 354

Qy      598 GCGCCATCCCTGCCGCCCCGCTGCCGCGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      355 GCGCCATCCCGCTGTCTGCTGCCGCGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      415 CCTCCGGCCCCGCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy      712 -----CCCGCCGCGCCCCCTTCCACGCCGCGCCGCGCCCAAGCGC 750
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCGCCCAAGCGC 534

Qy      751 AGGGGCTCC---GGCTCAGTGATGAGACCCTTTTTTGCTCTTCTGCTGCATCTGAGCCT 807
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      535 AGGGGCTCCTCGGGCTCAGTGATGAGACCCTTTTTTGCTCTTCTGCTGCATCTGAGCCT 594

Qy      808 GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      595 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651

Qy      868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGAACTGCTGCCTCTCTTCTTCT 927
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGAACTGCTGCCTCTCTTCTTCT 711

Qy      928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
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|    |      |   |      |
|----|------|---|------|
| Db | 772  | GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA  | 831  |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT  | 1107 |
| Db | 832  | GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC | 891  |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA  | 1167 |
| Db | 892  | TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA | 951  |
| Qy | 1168 | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT  | 1224 |
| Db | 952  | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT  | 1011 |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC            | 1269 |
| Db | 1012 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT  | 1071 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA  | 1329 |
| Db | 1072 | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA   | 1131 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA  | 1389 |
| Db | 1132 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA  | 1191 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG         | 1437 |
| Db | 1192 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG  | 1248 |
| Qy | 1438 | GAAAGTAAAGTGAGCAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG   | 1497 |
| Db | 1249 | GAAAGTAAAGTGAGTAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA  | 1308 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGAC    | 1557 |
| Db | 1309 | GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAGGAT   | 1368 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA  | 1614 |
| Db | 1369 | CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA  | 1428 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAACAGATGAAAAAAA   | 1674 |
| Db | 1429 | ACAAACATTTTTCCT125X6 GAGATCCTACTTCAGAAAAATAAGACCGATGAAAGGAT   | 1488 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT  | 1731 |
| Db | 1489 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC  | 1548 |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA  | 1791 |
| Db | 1549 | CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA  | 1608 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG  | 1851 |

Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668  
 Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 |||||  
 Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728  
 Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 |||||  
 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788  
 Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031  
 |||||  
 Db 1789 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1848  
 Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA 2091  
 |||||  
 Db 1849 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA 1908  
 Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151  
 || |||  
 Db 1909 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAAC 1965  
 Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208  
 |||||  
 Db 1966 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA 2025  
 Qy 2209 GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATA 2268  
 || |||  
 Db 2026 GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2085  
 Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC 2328  
 || |||||  
 Db 2086 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC 2145  
 Qy 2329 TCTAATTATTAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388  
 |||  
 Db 2146 TCTGATTATTAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT 2205  
 Qy 2389 GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTCCTGAA 2448  
 ||  
 Db 2206 GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC 2265  
 Qy 2449 GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A 2502  
 || |||||  
 Db 2266 GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA 2325  
 Qy 2503 GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562  
 |  
 Db 2326 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA 2385  
 Qy 2563 GGAAAGCCATATTTAGAGTCTTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619  
 |||||  
 Db 2386 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA 2445  
 Qy 2620 TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT 2679  
 || |||||  
 Db 2446 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC 2505

|    |      |   |      |
|----|------|---|------|
| Qy | 2680 | AATAC TGCAATTTATTCAAATGATGACTTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA  | 2739 |
| Db | 2506 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA    | 2565 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC    | 2799 |
| Db | 2566 | ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC    | 2625 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC    | 2856 |
| Db | 2626 | AGTTCATAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC   | 2685 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG    | 2916 |
| Db | 2686 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAATTG     | 2745 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCTTAAAGATGAAG-----TACATGTTTCA     | 2970 |
| Db | 2746 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA    | 2805 |
| Qy | 2971 | GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC    | 3030 |
| Db | 2806 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT    | 2865 |
| Qy | 3031 | TCTGCTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA     | 3090 |
| Db | 2866 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA    | 2925 |
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA    | 3150 |
| Db | 2926 | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA    | 2985 |
| Qy | 3151 | TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG    | 3210 |
| Db | 2986 | TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG    | 3045 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC   | 3270 |
| Db | 3046 | AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTTCAGC | 3105 |
| Qy | 3271 | ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG    | 3330 |
| Db | 3106 | ATTGTCAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG    | 3165 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA    | 3390 |
| Db | 3166 | ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA    | 3225 |
| Qy | 3391 | TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT    | 3450 |
| Db | 3226 | TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT    | 3285 |
| Qy | 3451 | CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA     | 3510 |
| Db | 3286 | CTTGGTCATGTGAACAGCATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA       | 3345 |







| Accession | Position | Sequence  | Position |
|-----------|----------|---|----------|
| Db        | 295      | CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC   | 354      |
| Qy        | 598      | GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCAGAGGACGACGAG   | 657      |
| Db        | 355      | GCGCCATCCCGTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG    | 414      |
| Qy        | 658      | CCTCCGGCGAGGCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----     | 711      |
| Db        | 415      | CCTCCGGCCCGGCCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG  | 474      |
| Qy        | 712      | -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC                  | 750      |
| Db        | 475      | TGGAACCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTTCCACCCCGCGCGCCCAAGCGC    | 534      |
| Qy        | 751      | AGGGGCTCC---GGCTCAGTGATGAGACCCCTTTTGTCTTCTCTGCTGCATCTGAGCCT   | 807      |
| Db        | 535      | AGGGGCTCCTCGGGCTCAGTGATGAGACCCCTTTTGTCTTCTCTGCTGCATCTGAGCCT   | 594      |
| Qy        | 808      | GTGATACCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAGCCAGGTAACACTGTT    | 867      |
| Db        | 595      | GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT   | 651      |
| Qy        | 868      | TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCCTCTCTTCCTTCT    | 927      |
| Db        | 652      | TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCCTCTCTTCCTTCT    | 711      |
| Qy        | 928      | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGAACCTTATCAGCA  | 987      |
| Db        | 712      | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGAATTTGTCAACA   | 771      |
| Qy        | 988      | GTGTCTATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA  | 1047     |
| Db        | 772      | GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA  | 831      |
| Qy        | 1048     | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT  | 1107     |
| Db        | 832      | GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAAACAGAGTTTTCAGAATTAGAATAC | 891      |
| Qy        | 1108     | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA  | 1167     |
| Db        | 892      | TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA  | 951      |
| Qy        | 1168     | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT  | 1224     |
| Db        | 952      | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT  | 1011     |
| Qy        | 1225     | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC            | 1269     |
| Db        | 1012     | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT  | 1071     |
| Qy        | 1270     | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCTAGTAGTA | 1329     |
| Db        | 1072     | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGAA    | 1131     |
| Qy        | 1330     | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA  | 1389     |

Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
 |||| | ||| | ||| ||| || ||||| ||| || ||

Db 1192 GATA--GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497  
 ||||| ||||| || ||||| || ||||| || ||||| || || || ||

Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1308

Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC 1557  
 ||||| || || ||||| || ||||| ||||| ||||| || || |||||

Db 1309 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1368

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT--CAGCAACCGAAAGCACCACA 1614  
 | | ||||| || ||||| ||||| | ||||| || |||ATATAT 3599

Db 1369 CGTCCAGGAGCATATATCATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1428

Qy 1615 GCAAACACTTTCCCTTTGTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAA 1674  
 ||||| || ||||| ||||| ||||| ||||| || ||||| |||||

Db 1429 ACAAACATTTTTCCTTTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAA 1488

Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG--ACTAGCCCCAAAACGTCAAAT 1731  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1489 ATAGAAGAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC 1548

Qy 1732 CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
 |||| | ||||| ||||| ||||| ||||| ||||| ||||| || || ||

Db 1549 CCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTAAACA 1608

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTACAG 1851  
 ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||

Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668

Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 ||||| ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||

Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 ||||| ||||| ||||| ||||| ||||| ||||| || || || || || || || ||

Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG 2031  
 ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1789 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCAACAGTTTTGCCTGACATTGTTATG 1848

Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA 2091  
 ||||| ||||| ||||| || || ||||| ||||| || || ||||| || || ||

Db 1849 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA 1908

Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151  
 || ||| | |||| || || ||||| ||||| || ||||| || ||||| |||||

Db 1909 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC 1965

Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208  
 ||||| ||||| ||||| ||||| ||||| ||||| || || || || || || || ||

Db 1966 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA 2025

|    |      |   |      |
|----|------|---|------|
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA   | 2268 |
|    |      |   |      |
| Db | 2026 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA    | 2085 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC   | 2328 |
|    |      |   |      |
| Db | 2086 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC   | 2145 |
| Qy | 2329 | TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCCGAACACGCTGAGCTAGTG   | 2388 |
|    |      |   |      |
| Db | 2146 | TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT    | 2205 |
| Qy | 2389 | GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA | 2448 |
|    |      |   |      |
| Db | 2206 | GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC   | 2265 |
| Qy | 2449 | GTCCACAAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A     | 2502 |
|    |      |   |      |
| Db | 2266 | GTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA     | 2325 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA    | 2562 |
|    |      |   |      |
| Db | 2326 | TTTGAGTCAATGATAGAATATGAAAAAAGGAAAAAAGTCTGCTTTGCCACCTGAGGGA      | 2385 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA    | 2619 |
|    |      |   |      |
| Db | 2386 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA    | 2445 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT    | 2679 |
|    |      |   |      |
| Db | 2446 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC    | 2505 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA    | 2739 |
|    |      |   |      |
| Db | 2506 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA    | 2565 |
| Qy | 2740 | AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC     | 2799 |
|    |      |   |      |
| Db | 2566 | ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC     | 2625 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC    | 2856 |
|    |      |   |      |
| Db | 2626 | AGTTCTAAAAGTGAATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC   | 2685 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG   | 2916 |
|    |      |   |      |
| Db | 2686 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAATTG     | 2745 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA     | 2970 |
|    |      |   |      |
| Db | 2746 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA    | 2805 |
| Qy | 2971 | GATGAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTC     | 3030 |
|    |      |   |      |
| Db | 2806 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT    | 2865 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3031 | TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA   | 3090 |
|    |      |  |      |
| Db | 2866 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA   | 2925 |
| Qy | 3091 | GAAGCAGAGAAAAAATTCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA     | 3150 |
|    |      |  |      |
| Db | 2926 | GAAGCTGAGAAAAAATTCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA     | 2985 |
| Qy | 3151 | TTGTCAGCAGAGCTGAGTAAAATTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG   | 3210 |
|    |      |  |      |
| Db | 2986 | TTTTCAGCAGAGCTGAGTAAAATTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG   | 3045 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGCTCTGACAGTGTTTCAGC  | 3270 |
|    |      |  |      |
| Db | 3046 | AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC  | 3105 |
| Qy | 3271 | ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG   | 3330 |
|    |      |  |      |
| Db | 3106 | ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG   | 3165 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3390 |
|    |      |  |      |
| Db | 3166 | ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3225 |
| Qy | 3391 | TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT  | 3450 |
|    |      |  |      |
| Db | 3226 | TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCTGCT | 3285 |
| Qy | 3451 | CTTGGTCATGTGAACAGCACAAATAAAGAAGTGAAGCGGCTTTTCTTAGTTGATGATTTA   | 3510 |
|    |      |  |      |
| Db | 3286 | CTTGGTCATGTGAAGTGCACGATAAAGGAAGTGAAGCGGCTTTTCTTAGTTGATGATTTA   | 3345 |
| Qy | 3511 | GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT   | 3570 |
|    |      |  |      |
| Db | 3346 | GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT   | 3405 |
| Qy | 3571 | AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT   | 3630 |
|    |      |  |      |
| Db | 3406 | AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT   | 3465 |
| Qy | 3631 | GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT   | 3690 |
|    |      |  |      |
| Db | 3466 | GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAGAT    | 3525 |
| Qy | 3691 | GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA             | 3740 |
|    |      |  |      |
| Db | 3526 | GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA             | 3575 |

RESULT 12

AAD01174

ID AAD01174 standard; cDNA; 3833 BP.

XX

AC AAD01174;

XX

DT 02-NOV-2000 (first entry)

XX

DE Bovine neurite growth inhibitor Nogo cDNA.

XX

KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening; ss.

XX

OS Bos sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating eoplastic 5

PT disorders of the central nervous system and inducing regeneration of

PT neurons -

XX

PS Claim 26; Fig 12; 122pp; English.

XX

CC The present sequence is a cDNA encoding bovine Nogo protein which is a

CC potent neural cell growth inhibitor and is free of all central nervous

CC system (CNS) myelin material with which it is natively associated. The

CC present sequence was obtained from bovine spinal cord white matter cDNA

CC library. Nogo proteins and fragments displaying neurite growth inhibitory

CC activity are used in the treatment of neoplastic disease of the CNS

CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,

CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,

CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve

CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which

CC promo Nogo activity can be used to treat or prevent hyperproliferative

CC or benign dysproliferative disorders e.g. psoriasis and tissue

CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to

CC inhibit production of Nogo protein to induce regeneration of neurons or

CC to promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired.

CC The animal models can be used in diagnostic and screening methods for

CC predisposition to disorders and to screen for or test molecules which

CC can treat or prevent disorders or diseases of the CNS.

CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29

CC in disclosure of the specification. However the specification does not

CC include sequences for these SEQ ID numbers.

XX

SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 other;

Query Match 50.0%; Score 1869.8; DB 21; Length 3833;  
Best Local Similarity 80.9%; Pred. No. 0;  
Matches 2320; Conservative 0; Mismatches 492; Indels 55; Gaps 10;

|    |      |  |      |
|----|------|--|------|
| Qy | 928  | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA  | 987  |
|    |      |  |      |
| Db | 1    | CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA    | 60   |
|    |      |  |      |
| Qy | 988  | GTGTCAATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA   | 1047 |
|    |      |  |      |
| Db | 61   | GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA   | 120  |
|    |      |  |      |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAAATTAGAATAT  | 1107 |
|    |      |  |      |
| Db | 121  | GAGAAGGCACAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAAATTGGAATAT | 180  |
|    |      |  |      |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA   | 1167 |
|    |      |  |      |
| Db | 181  | TCAGAAATGGAATCATCATTCACTGAGGCTCTCAAAGGCAGAACCTGCCGTAAACAGTAGCG | 240  |
|    |      |  |      |
| Qy | 1168 | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT   | 1224 |
|    |      |  |      |
| Db | 241  | AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT   | 300  |
|    |      |  |      |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA                | 1266 |
|    |      |  |      |
| Db | 301  | AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA   | 360  |
|    |      |  |      |
| Qy | 1267 | GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTA   | 1326 |
|    |      |  |      |
| Db | 361  | GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA    | 420  |
|    |      |  |      |
| Qy | 1327 | GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG   | 1386 |
|    |      |  |      |
| Db | 421  | GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG   | 480  |
|    |      |  |      |
| Qy | 1387 | AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT-----          | 1434 |
|    |      |  |      |
| Db | 481  | AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA   | 540  |
|    |      |  |      |
| Qy | 1435 | GTGGAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGG     | 1494 |
|    |      |  |      |
| Db | 541  | TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAAACAAACAAATCGTGAA  | 600  |
|    |      |  |      |
| Qy | 1495 | AAGGATAGTGAAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAG   | 1554 |
|    |      |  |      |
| Db | 601  | AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA    | 660  |
|    |      |  |      |
| Qy | 1555 | GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA   | 1614 |
|    |      |  |      |
| Db | 661  | GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACCTGAGAATGTTTCA  | 720  |
|    |      |  |      |
| Qy | 1615 | GCAAACACTTTCCCTTTGTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA  | 1674 |
|    |      |  |      |
| Db | 721  | ACAAACATTTTCCCTTGTGTTGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAAAG   | 780  |

|    |      |   |      |
|----|------|---|------|
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA--CTAGCCCCAAAACGTCAAAT   | 1731 |
|    |      |   |      |
| Db | 781  | ATAGAA-AAAAAAGGCACAAATTGTAAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC  | 839  |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA  | 1791 |
|    |      |   |      |
| Db | 840  | CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA  | 899  |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG | 1851 |
|    |      |   |      |
| Db | 900  | AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTTCAG  | 959  |
| Qy | 1852 | GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA  | 1911 |
|    |      |   |      |
| Db | 960  | GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA  | 1019 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT   | 1971 |
|    |      |   |      |
| Db | 1020 | ATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT | 1079 |
| Qy | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCGTGATATTGTTATG | 2031 |
|    |      |   |      |
| Db | 1080 | TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCGTGACATTGTCATG  | 1139 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA  | 2091 |
|    |      |   |      |
| Db | 1140 | GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA  | 1199 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC  | 2151 |
|    |      | c   | 13   |
| Db | 1200 | TCACCATTAGAAACTCTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAT   | 1259 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA  | 2208 |
|    |      |   |      |
| Db | 1260 | CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA   | 1319 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA | 2268 |
|    |      |   |      |
| Db | 1320 | GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA | 1379 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC | 2328 |
|    |      |   |      |
| Db | 1380 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC | 1439 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG | 2388 |
|    |      |   | 791  |
| Db | 1440 | TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT | 1499 |
| Qy | 2389 | GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA  | 2448 |
|    |      |   |      |
| Db | 1500 | GAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA   | 1559 |
| Qy | 2449 | GTCCCAAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC-   | 2507 |
|    |      |   |      |
| Db | 1560 | GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA  | 1619 |
| Qy | 2508 | -----TGAGACAGTAGCCCAGCACAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG   | 2559 |



|    |      |  |      |
|----|------|--|------|
| Db | 1620 | TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAG   | 1679 |
| Qy | 2560 | CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC--T    | 2616 |
| Db | 1680 | GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAACCTTA  | 1739 |
| Qy | 2617 | GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAG  | 2676 |
| Db | 1740 | GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAG  | 1799 |
| Qy | 2677 | TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA   | 2736 |
| Db | 1800 | CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA   | 1859 |
| Qy | 2737 | GAAAGTGAAACATTTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTT  | 2796 |
| Db | 1860 | GAAAGTGAAACATTTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT | 1919 |
| Qy | 2797 | GTCAGTGCTAA--AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA    | 2853 |
| Db | 1920 | GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA   | 1979 |
| Qy | 2854 | TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGAGATTTCATTGCCTTGCTTAGAA   | 2913 |
| Db | 1980 | GCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGA    | 2039 |
| Qy | 2914 | TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT   | 2973 |
| Db | 2040 | TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT    | 2099 |
| Qy | 2974 | GAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT   | 3033 |
| Db | 2100 | GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGTGCCCGTACTGCCTCCAGATGTTTCT    | 2159 |
| Qy | 3034 | GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA   | 3093 |
| Db | 2160 | GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCCTGTGAAAGAA   | 2219 |
| Qy | 3094 | GCAGAGAAAAAATTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGTATTG      | 3153 |
| Db | 2220 | GCCGAGAGAAAAATTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT   | 2279 |
| Qy | 3154 | TCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG    | 3213 |
| Db | 2280 | TCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG    | 2339 |
| Qy | 3214 | ACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATT  | 3273 |
| Db | 2340 | ACTGGAGTGGTGTTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTTCAGCATT   | 2399 |
| Qy | 3274 | GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA   | 3333 |
| Db | 2400 | GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATA     | 2459 |
| Qy | 3334 | TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATAT   | 3393 |

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Db      2460 TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTGAGGGCATAT 2519
Qy      3394 TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT 3453
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2520 TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT 2579
Qy      3454 GGTTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2580 GGTTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT 2639
Qy      3514 GATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC AAT 3573
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2640 GATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTC AAT 2699
Qy      3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA 3633
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2700 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA 2759
Qy      3634 CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC 3693
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2760 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT 2819
Qy      3694 ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2820 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA 2866

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# RESULT 13

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

XX

AC AAV30920;

XX

DT 14-SEP-1998 (first entry)

XX

DE Human secreted protein BG160\_1 cDNA.

XX

KW BG160\_1; secreted protein; protein factor; human; ds.

XX

OS Homo sapiens.

XX

|    |     |                     |  |
|----|-----|---------------------|--|
| FH | Key | Location/Qualifiers |  |
|----|-----|---------------------|--|

|    |     |           |  |
|----|-----|-----------|--|
| FT | CDS | 102..275X |  |
|----|-----|-----------|--|

|    |  |          |  |
|----|--|----------|--|
| FT |  | /*tag= a |  |
|----|--|----------|--|

|    |             |            |  |
|----|-------------|------------|--|
| FT | sig_peptide | 1863..1899 |  |
|----|-------------|------------|--|

|    |  |          |  |
|----|--|----------|--|
| FT |  | /*tag= b |  |
|----|--|----------|--|

|    |  |   |  |
|----|--|---|--|
| FT |  | /note= "putative leader/signal peptide" |  |
|----|--|---|--|

|    |             |            |  |
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| FT | mat_peptide | 1900..2027 |  |
|----|-------------|------------|--|

|    |  |          |  |
|----|--|----------|--|
| FT |  | /*tag= c |  |
|----|--|----------|--|

XX

PN WO9817687-A2.

XX

PD 30-APR-1998.

XX

PF 24-OCT-1997; 97WO-US19590.

XX

PR 24-OCT-1997; 97US-0740274.

PR 25-OCT-1996; 96US-0740274.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
 PI Racie LA, Spaulding V, Treacy M;  
 XX  
 DR WPI; 1998-261426/23.  
 DR P-PSDB; AAW58383.  
 XX  
 PT Nucleic acid encoding secreted protein from human cells - useful,  
 PT e.g. as immunomodulator, antitumour agent, promoters of tissue  
 PT growth, haemostatic and thrombolytic agents etc.  
 XX  
 PS Claim 20; Page 74-75; 114pp; English.  
 XX  
 CC This cDNA clone, designated BG160\_1, codes for a novel human  
 CC secreted protein (see AAW58383). It was isolated from a human adult  
 CC brain cDNA library using methods selective for cDNAs that encode  
 CC secreted proteins. The clone is deposited in composite clone  
 CC ATCC 98232; an oligonucleotide (see AAT99725) is designed to isolate  
 CC the clone from the composite. The predicted AT415\_4 amino acid  
 CC sequence shows homology to neuroendocrine-specific proteins. Novel  
 CC cDNA clones (see AAV30916-32) coding for human secreted proteins (see  
 CC AAW58580-90) are claimed. These can be used for recombinant  
 CC production of the secreted proteins for analysis, characterisation,  
 CC diagnostic or therapeutic use. They can also be used as tissue or  
 CC mol.wt. markers, for chromosome identification, to identify genetic  
 CC disorders, to isolate new related DNA, as sources of primers for  
 CC PCR, to generate antibodies, and in interaction trap assays. The  
 CC secreted proteins may also have many biological activities, e.g.  
 CC cytokine, immunomodulator, haematopoiesis regulating activity,  
 CC tissue growth activity, activin or inhibin activity, chemotactic or  
 CC chemokinetic activity, haemostatic and thrombolytic activity,  
 CC receptor/ligand activity, antiinflammatory, cadherin and tumour  
 CC invasion suppressor activity, and tumour inhibition activity. The  
 CC proteins can be expressed in vivo from DNA, introduced in gene  
 CC therapy vectors.  
 XX  
 SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 other;

Query Match 37.7%; Score 1411.2; DB 19; Length 2386;  
 Best Local Similarity 83.3%; Pred. No. 1.4e-289;  
 Matches 1702; Conservative 0; Mismatches 303; Indels 39; Gaps 7;

Qy 1718 CAAAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAA 1777  
 ||||| |||| |||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1 CAAAACATCAAACCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAA 60  
 Qy 1778 CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC 1837  
 ||||| ||| ||||| ||||| || ||| ||||| ||||| ||||| |||||  
 Db 61 CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC 120  
 Qy 1838 CAGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTG 1897  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 121 CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG 180

|    |      |                     |   |      |
|----|------|---------------------|---|------|
| Qy | 1898 | CTTATGAAACAAAAGTGGA | CTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACC         | 1957 |
| Db | 181  | CTTATGAAACAAAATGGA  | CTTGGTCAAACATCAGAAGTTATGCAAGAGTCACTCTATC          | 240  |
| Qy | 1958 | CCACAGCACAGCTTTGCC  | CATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTC         | 2017 |
| Db | 241  | CTGCAGCACAGCTTTGCC  | CATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTC         | 300  |
| Qy | 2018 | CTGATATTGTTATGGAAG  | CACCATTAATTTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAG        | 2077 |
| Db | 301  | CTGACATTGTTATGGAAG  | CACCATTAATTTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGA        | 360  |
| Qy | 2078 | TGCAGCCCAGTGTATCCCC | ACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGC         | 2137 |
| Db | 361  | TACAGC              | CTCATCACCAATAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAC | 417  |
| Qy | 2138 | TTGAGCCTGAAAAACCCCC | ACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTT         | 2194 |
| Db | 418  | ATGAGCCTGAAAAACCCCC | ACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTAT          | 477  |
| Qy | 2195 | TGGGAACAAAGGAAGGA   | ATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAAGAAACAG      | 2254 |
| Db | 478  | CAGGAATAAAGGAAGAA   | ATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAG        | 537  |
| Qy | 2255 | AAGCTCCTTATATATCC   | ATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGC       | 2314 |
| Db | 538  | AAGCTCCTTATATATCT   | ATTGCGTGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAAC        | 597  |
| Qy | 2315 | CAAGTCCAGATTTCTCT   | AAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAAC      | 2374 |
| Db | 598  | CAGCTCCGATTTCTCT    | GATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATC       | 657  |
| Qy | 2375 | ACGCTGAGCTAGTGGAG   | GATTCTCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATG      | 2434 |
| Db | 658  | ATTCTGAGCTAGTTGA    | AGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATG     | 717  |
| Qy | 2435 | ATTTCGATTCTTGAAGT   | CCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTC      | 2494 |
| Db | 718  | ATTCAATACCTGACGTT   | CCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTC       | 777  |
| Qy | 2495 | TCAGTGA-----AGT     | GTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCTT       | 2548 |
| Db | 778  | TCAGTGAAGCTTCATT    | TGAGTCAATGATAGAATATGAAATAAGGAAAAACTCAGTGCTT       | 837  |
| Qy | 2549 | CACCTCAGGAGCTAGGA   | AGCCATATTTAGAGTCTTTTTAGCCCAATTTACATAGTACAA        | 2608 |
| Db | 838  | TGCCACCTGAGGGAGGA   | AGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAA        | 897  |
| Qy | 2609 | AAGATGC---TGCATCT   | AATGACATTCCACATTGACCAAAAAGGAGAAAAATTTCTTTTC       | 2665 |
| Db | 898  | AAGATACCTGTTACCT    | GATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTTC      | 957  |
| Qy | 2666 | AAATGGAAGAGTTTA     | ATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAG     | 2725 |
| Db | 958  | AGATGGAGGAGCTCAG    | TACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAG      | 1017 |
| Qy | 2726 | ACAAAATAAAAAGAA     | AGTGAAACATTTTTCAGATTTCATCTCCGATTGAGATAATAGATGAAT  | 2785 |

| Accession | Query | Reference   | Score | Identical | Mismatch | Gap | Start | End  |
|-----------|-------|---|-------|-----------|----------|-----|-------|------|
| Db        | 1018  | CACAGATAAGAGAAAACCTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGT | 1077  | 100       | 0        | 0   | 1     | 1077 |
| Qy        | 2786  | TTCCACGTTTGTCTAGTGCTAAAGATGATTC--TCCTAAATTAGCCAAGGAGTACACTG     | 2842  | 100       | 0        | 0   | 1     | 2842 |
| Db        | 1078  | TCCCTACATTGATCAGTTCTAAAACCTGATTCAATTTCTAAATTAGCCAGGGAATATACTG   | 1137  | 100       | 0        | 0   | 1     | 1137 |
| Qy        | 2843  | ATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGC   | 2902  | 100       | 0        | 0   | 1     | 2902 |
| Db        | 1138  | ACCTAGAAGTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGC      | 1199  | 100       | 0        | 0   | 1     | 1199 |
| Qy        | 2903  | CTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG---    | 2959  | 100       | 0        | 0   | 1     | 2959 |
| Db        | 1198  | CTTGACAGAAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGA     | 1257  | 100       | 0        | 0   | 1     | 1257 |
| Qy        | 2960  | ---TACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATAT    | 3016  | 100       | 0        | 0   | 1     | 3016 |
| Db        | 1258  | AAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTAT    | 1317  | 100       | 0        | 0   | 1     | 1317 |
| Qy        | 3017  | CGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCA    | 3076  | 100       | 0        | 0   | 1     | 3076 |
| Db        | 1318  | TGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCA    | 1377  | 100       | 0        | 0   | 1     | 1377 |
| Qy        | 3077  | AATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGAT    | 3136  | 100       | 0        | 0   | 1     | 3136 |
| Db        | 1378  | AAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGAT    | 1437  | 100       | 0        | 0   | 1     | 1437 |
| Qy        | 3137  | CCCTGTCTAGCTGTATTGTCTGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACT | 3196  | 100       | 0        | 0   | 1     | 3196 |
| Db        | 1438  | CCCTGTCTAGCTGTATTGTCTGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACT | 1497  | 100       | 0        | 0   | 1     | 1497 |
| Qy        | 3197  | GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTGTCTC    | 3256  | 100       | 0        | 0   | 1     | 3256 |
| Db        | 1498  | GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTTTTCTAT  | 1557  | 100       | 0        | 0   | 1     | 1557 |
| Qy        | 3257  | TGACAGTGTTCAGCATTGTCTAGTGTAACGGCTACATTGCCTTGGCCCTGCTCTCGGTGA    | 3316  | 100       | 0        | 0   | 1     | 3316 |
| Db        | 1558  | TGACAGTATTCTAGCATTGTCTAGTGTAACGGCTACATTGCCTTGGCCCTGCTCTCTGTGA   | 1617  | 100       | 0        | 0   | 1     | 1617 |
| Qy        | 3317  | CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC    | 3376  | 100       | 0        | 0   | 1     | 3376 |
| Db        | 1618  | CCATCAGCTTTAGGATATACAAGGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC   | 1677  | 100       | 0        | 0   | 1     | 1677 |
| Qy        | 3377  | ACCCATTACAGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAAT   | 3436  | 100       | 0        | 0   | 1     | 3436 |
| Db        | 1678  | ACCCATTACAGG---GAAGTTGCTATATCTGAGGAGTTGGTTGAGAAGT               | 3722  | 100       | 0        | 0   | 1     | 3722 |
| Qy        | 3437  | ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAGAAGCTGAGGCGGCTTTTCT   | 3496  | 100       | 0        | 0   | 1     | 3496 |
| Db        | 1723  | ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACGATAAAGGAAGCTGAGGCGGCTCTTCT   | 1782  | 100       | 0        | 0   | 1     | 1782 |
| Qy        | 3497  | TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGACAGTGTGATGTGGGTGTTTACTTATG    | 3556  | 100       | 0        | 0   | 1     | 3556 |
| Db        | 1783  | TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGACAGTGTGATGTGGGTATTTACCTATG    | 1842  | 100       | 0        | 0   | 1     | 1842 |
| Qy        | 3557  | TTGGTGCCTTGTTCATGTTGCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA    | 3616  | 100       | 0        | 0   | 1     | 3616 |

Db 1843 TTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 1902  
 Qy 3617 TTCCTGTTATTTATGAACGGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676  
 Db 1903 TTCCTGTTATTTATGAACGGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 1962  
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736  
 Db 1963 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 2022  
 Qy 3737 CAGA 3740  
 Db 2023 CTGA 2026

# RESULT 14

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX

AC AAF98399;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone BG160\_1 sequence SEQ ID 41.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;  
 KW differentiation; immune system modulator; tissue growth; chemotactic;  
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;  
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US25135.

XX

PR 17-SEP-1999; 99US-0398829.

XX

PA (GEMY ) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

XX

DR WPI; 2001-244801/25.

DR P-PSDB; AAB90682.

XX

PT Isolated nucleic acids encoding polypeptides, useful for modulating  
 PT e.g. cytokine and cell proliferation/differentiation activity, the  
 PT immune system and hematopoiesis regulating activity -

XX

PS Claim 1; Page 408-409; 557pp; English.

XX

CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various  
 CC tissue types, and may be used in the prevention, treatment and diagnosis



|    |      |  |      |
|----|------|--|------|
| Db | 538  | AAGCTCCTTATATATCTATTGCGATGTGATTAAATTAAGAAACAAAGCTTTCTGCTGAAC   | 597  |
| Qy | 2315 | CAAGTCCAGATTTCTCTAATTATTGAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAAC   | 2374 |
|    |      |  |      |
| Db | 598  | CAGCTCCGATTTCTCTGATTATTGAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATC    | 657  |
| Qy | 2375 | ACGCTGAGCTAGTGGAGGATTCTCACCCTGAATCTGAACCAGTTGACTTATTTAGTGATG   | 2434 |
|    |      |  |      |
| Db | 658  | ATTCTGAGCTAGTTGAAGATTCTCACCCTGATTCTGAACCAGTTGACTTATTTAGTGATG   | 717  |
| Qy | 2435 | ATTGATTCTGAAGTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTC      | 2494 |
|    |      |  |      |
| Db | 718  | ATTCAATACCTGACGTTCCACAAACCAAGATGAAACTGTGATGCTTGTGAAAGAAAGTC    | 777  |
| Qy | 2495 | TCAGTGA-----AGTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCTT     | 2548 |
|    |      |  |      |
| Db | 778  | TCAGTGAAGTTCATTTGAGTCAATGATAGAAATATGAAATAAGGAAAACTCAGTGCTT     | 837  |
| Qy | 2549 | CACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAA   | 2608 |
|    |      |  |      |
| Db | 838  | TGCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAA   | 897  |
| Qy | 2609 | AAGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGC  | 2665 |
|    |      |  |      |
| Db | 898  | AAGATACCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGC   | 957  |
| Qy | 2666 | AAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAG   | 2725 |
|    |      |  |      |
| Db | 958  | AGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAG   | 1017 |
| Qy | 2726 | ACAAAATAAAAAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAAT | 2785 |
|    |      |  |      |
| Db | 1018 | CACAGATAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATATAGATGAGT   | 1077 |
| Qy | 2786 | TTCCACGTTTGTCAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTG    | 2842 |
|    |      |  |      |
| Db | 1078 | TCCCTACATTGATCAGTTCTAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTG   | 1137 |
| Qy | 2843 | ATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAGCGGGGCAGATTCAATTGC   | 2902 |
|    |      |  |      |
| Db | 1138 | ACCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGC    | 1197 |
| Qy | 2903 | CTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG---   | 2959 |
|    |      |  |      |
| Db | 1198 | CTTGACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGA    | 1257 |
| Qy | 2960 | ---TACATGTTTCAGATGAATTCTCCGAAATAGGTCCAGTGTATCTAAGGCATCCATAT    | 3016 |
|    |      |  |      |
| Db | 1258 | AAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGTGCTCTTAT    | 1317 |
| Qy | 3017 | CGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCA   | 3076 |
|    |      |  |      |
| Db | 1318 | TGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCA   | 1377 |
| Qy | 3077 | AATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGAT   | 3136 |
|    |      |  |      |
| Db | 1378 | AAGTTCTTGTAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGAT     | 1437 |



|    |      |  |      |
|----|------|--|------|
| Qy | 3137 | CCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACT   | 3196 |
|    |      |  |      |
| Db | 1438 | CACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACT   | 1497 |
| Qy | 3197 | GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC  | 3256 |
|    |      |  |      |
| Db | 1498 | GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCAT | 1557 |
| Qy | 3257 | TGACAGTGTTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA | 3316 |
|    |      |  |      |
| Db | 1558 | TGACAGTATTTCAGCATTGTGAGCGTAAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA | 1617 |
| Qy | 3317 | CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC   | 3376 |
|    |      |  |      |
| Db | 1618 | CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC   | 1677 |
| Qy | 3377 | ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAAT | 3436 |
|    |      |  |      |
| Db | 1678 | ACCCATTTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAT           | 1722 |
| Qy | 3437 | ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT    | 3496 |
|    |      |  |      |
| Db | 1723 | ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGCCTCTTCT    | 1782 |
| Qy | 3497 | TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCACTGTTGATGTGGGTGTTTACTTATG   | 3556 |
|    |      |  |      |
| Db | 1783 | TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATG   | 1842 |
| Qy | 3557 | TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA   | 3616 |
|    |      |  |      |
| Db | 1843 | TTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG  | 1902 |
| Qy | 3617 | TTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA    | 3676 |
|    |      |  |      |
| Db | 1903 | TTGGTGTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA    | 1962 |
| Qy | 3677 | AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG   | 3736 |
|    |      |  |      |
| Db | 1963 | AGAATGTTAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG    | 2022 |
| Qy | 3737 | CAGA   | 3740 |
|    |      |  |      |
| Db | 2023 | CTGA   | 2026 |

# RESULT 15

AAI98079

ID AAI98079 standard; cDNA; 1980 BP.

XX

AC AAI98079;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human neuroblastoma expressed polynucleotide SEQ ID NO 22.

XX

KW Human; neuroblastoma; ss.

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XX      OS      Homo sapiens.
XX
XX      PN      WO200166733-A1.
XX
XX      PD      13-SEP-2001.
XX
XX      PF      02-MAR-2001; 2001WO-JP01631.
XX
XX      PR      07-MAR-2000; 2000JP-0159195.
XX      PR      12-MAY-2000; 2000JP-0140387.
XX
XX      PA      (CHIB-) CHIBA PREFECTURE.
XX      PA      (HISM ) HISAMITSU PHARM CO LTD.
XX
XX      PI      Nakagawara A;
XX
XX      DR      WPI; 2001-602630/68.
XX
XX      PT      Nucleic acids for prognosis of human neuroblastoma comprise nucleic
XX      PT      acids expressed by human neuroblastomas -
XX
XX      PS      Claim 1; Page 69-70; 159pp; Japanese.
XX
XX      CC      The invention relates to nucleic acids (AAI98058-AAI98161) or their
XX      CC      homologues expressed by human neuroblastomas useful for detecting genes
XX      CC      expressed by neuroblastoma and for analysing their structure and
XX      CC      function. The nucleic acids are useful for the diagnosis and prognosis of
XX      CC      neuroblastoma.
XX
XX      SQ      Sequence 1980 BP; 601 A; 373 C; 423 G; 583 T; 0 other;

Query Match          29.1%;  Score 1088.8;  DB 22;  Length 1980;
Best Local Similarity 83.5%;  Pred. No. 3.7e-221;
Matches 1289;  Conservative  0;  Mismatches 237;  Indels  18;  Gaps  4;

Qy      2215 AAAGAGCCTGAAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATT 2274
        |||
Db      28 AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT 87

Qy      2275 GCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAAT 2334
        ||
Db      88 GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGAT 147

Qy      2335 TATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGAT 2394
        |||
Db      148 TATTCAGAAATGGCAAAAGTTGAACAGCCAGTCCTGATCATTCTGAGCTAGTTGAAGAT 207

Qy      2395 TCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAAGTCCCA 2454
        |||
Db      208 TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA 267

Qy      2455 CAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----AGTGTCT 2508
        |||
Db      268 CAAAAACAAGCTGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTGAG 327

Qy      2509 GAGACAGTAGCCACGACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAAG 2568

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|    |      |  |      |
|----|------|--|------|
| Db | 328  | TCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAAG   | 387  |
| Qy | 2569 | CCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCATCTAAT   | 2625 |
| Db | 388  | CCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGAT   | 447  |
| Qy | 2626 | GACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACT   | 2685 |
| Db | 448  | GAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACT   | 507  |
| Qy | 2686 | GCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAA   | 2745 |
| Db | 508  | GCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAA   | 567  |
| Qy | 2746 | ACATTTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCTAGTGCT | 2805 |
| Db | 568  | ACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTTACATTGATCAGTCCT  | 627  |
| Qy | 2806 | AAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA   | 2862 |
| Db | 628  | AAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCACAAA     | 687  |
| Qy | 2863 | AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGT  | 2922 |
| Db | 688  | AGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAAATTGCCCCAT  | 747  |
| Qy | 2923 | GACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCAGATGAA    | 2976 |
| Db | 748  | GACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGAC   | 807  |
| Qy | 2977 | TTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCT    | 3036 |
| Db | 808  | TTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCT    | 867  |
| Qy | 3037 | TTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCA   | 3096 |
| Db | 868  | TTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCT   | 927  |
| Qy | 3097 | GAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCA   | 3156 |
| Db | 928  | GAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCA   | 987  |
| Qy | 3157 | GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACT   | 3216 |
| Db | 988  | GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACT   | 1047 |
| Qy | 3217 | GGAGTGGTGTTTGGTGCCAGCTTATTTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTC | 3276 |
| Db | 1048 | GGAGTGGTGTTTGGTGCCAGCCTATTCCAGCTGCTTTTCATTGACAGTATTCAGCATTGTC  | 1107 |
| Qy | 3277 | AGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATAT   | 3336 |
| Db | 1108 | AGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC   | 1167 |
| Qy | 3337 | AAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGCATATTTA    | 3396 |

|    |      |   |               |      |
|----|------|---|---------------|------|
| Db | 1168 | AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATT               | CAGGGCATATCTG | 1227 |
| Qy | 3397 | GAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGT  |               | 3456 |
|    |      |   |               |      |
| Db | 1228 | GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT  |               | 1287 |
| Qy | 3457 | CATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT |               | 3516 |
|    |      |   |               |      |
| Db | 1288 | CATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT  |               | 1347 |
| Qy | 3517 | TCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGT  |               | 3576 |
|    |      |   |               |      |
| Db | 1348 | TCTCTGGAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGT |               | 1407 |
| Qy | 3577 | CTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGG  |               | 3636 |
|    |      |   |               |      |
| Db | 1408 | CTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGG  |               | 1467 |
| Qy | 3637 | CATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATG  |               | 3696 |
|    |      |   |               |      |
| Db | 1468 | CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG  |               | 1527 |
| Qy | 3697 | GCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA                  |               | 3740 |
|    |      |   |               |      |
| Db | 1528 | GCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA                  |               | 1571 |

Search completed: January 23, 2004, 03:14:18  
Job time : 913.477 secs

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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:43:47 ; Search time 189.668 Seconds  
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8705.823 Million cell updates/sec

Title: US-09-830-972-1  
Perfect score: 3741  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result |     |        | %     |         | Query |                    |  |                   | Description |
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| c      | 8   | 75.4   | 2.0   | 7218    | 1     | US-08-232-463-14   |  | Sequence 14, Appl |             |
|        | 9   | 75.2   | 2.0   | 152331  | 3     | US-09-128-155-16   |  | Sequence 16, Appl |             |
| c      | 10  | 74.6   | 2.0   | 2481    | 4     | US-09-894-998A-35  |  | Sequence 35, Appl |             |
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| c | 12 | 73.2 | 2.0 | 4411529 | 3 | US-09-103-840A-1    | Sequence 1, Appli |
| c | 13 | 68.6 | 1.8 | 319     | 3 | US-09-165-264-8     | Sequence 8, Appli |
|   | 14 | 68   | 1.8 | 4403765 | 3 | US-09-103-840A-2    | Sequence 2, Appli |
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| c | 16 | 67.8 | 1.8 | 320     | 3 | US-09-165-264-13    | Sequence 13, Appl |
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|   | 18 | 67.6 | 1.8 | 15378   | 3 | US-08-785-420-1     | Sequence 1, Appli |
| c | 19 | 67.4 | 1.8 | 4600    | 4 | US-09-702-705-1797  | Sequence 1797, Ap |
| c | 20 | 67.4 | 1.8 | 4600    | 4 | US-09-736-457-1797  | Sequence 1797, Ap |
| c | 21 | 66.8 | 1.8 | 320     | 3 | US-09-165-264-11    | Sequence 11, Appl |
| c | 22 | 65.8 | 1.8 | 320     | 3 | US-09-165-264-14    | Sequence 14, Appl |
| c | 23 | 64.6 | 1.7 | 318     | 3 | US-09-165-264-12    | Sequence 12, Appl |
| c | 24 | 64.6 | 1.7 | 8438    | 1 | US-07-945-283-1     | Sequence 1, Appli |
| c | 25 | 63.8 | 1.7 | 1926    | 4 | US-09-249-585A-4    | Sequence 4, Appli |
| c | 26 | 63.8 | 1.7 | 1931    | 2 | US-09-130-114-2     | Sequence 2, Appli |
|   | 27 | 63.6 | 1.7 | 4041    | 3 | US-09-105-537-36    | Sequence 36, Appl |
|   | 28 | 63.6 | 1.7 | 36778   | 3 | US-09-105-537-5     | Sequence 5, Appli |
|   | 29 | 63.6 | 1.7 | 38506   | 3 | US-09-320-878-19    | Sequence 19, Appl |
|   | 30 | 63.6 | 1.7 | 38506   | 4 | US-09-141-908-1     | Sequence 1, Appli |
|   | 31 | 63.6 | 1.7 | 38506   | 4 | US-09-657-440-19    | Sequence 19, Appl |
|   | 32 | 61.6 | 1.6 | 8438    | 1 | US-07-945-283-1     | Sequence 1, Appli |
|   | 33 | 60.8 | 1.6 | 2109    | 4 | US-09-370-838-153   | Sequence 153, App |
| c | 34 | 60.6 | 1.6 | 1776    | 1 | US-08-722-001-29    | Sequence 29, Appl |
|   | 35 | 60.6 | 1.6 | 4257    | 2 | US-08-690-473-1     | Sequence 1, Appli |
|   | 36 | 60.6 | 1.6 | 4257    | 3 | US-09-259-821A-1    | Sequence 1, Appli |
|   | 37 | 60.6 | 1.6 | 4257    | 3 | US-08-843-659-1     | Sequence 1, Appli |
| c | 38 | 60.6 | 1.6 | 12001   | 1 | US-08-458-568A-11   | Sequence 11, Appl |
|   | 39 | 60   | 1.6 | 2301    | 1 | US-08-306-691B-23   | Sequence 23, Appl |
|   | 40 | 60   | 1.6 | 2301    | 4 | US-09-167-206-3     | Sequence 3, Appli |
|   | 41 | 60   | 1.6 | 2301    | 5 | PCT-US93-06251-78   | Sequence 78, Appl |
| c | 42 | 59.4 | 1.6 | 426     | 4 | US-09-252-991A-6856 | Sequence 6856, Ap |
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|   | 44 | 59.4 | 1.6 | 570     | 4 | US-09-252-991A-6898 | Sequence 6898, Ap |
|   | 45 | 59.4 | 1.6 | 723     | 4 | US-09-252-991A-6936 | Sequence 6936, Ap |

#### ALIGNMENTS

##### RESULT 1

US-09-484-970B-106

; Sequence 106, Application US/09484970B

; Patent No. 6426186

; GENERAL INFORMATION:

; APPLICANT: Jones, Karen A.

; APPLICANT: Volkmuth, Wayne

; APPLICANT: Walker, Michael G.

; TITLE OF INVENTION: BONE REMODELING GENES

; FILE REFERENCE: PB-0014 US

; CURRENT APPLICATION NUMBER: US/09/484,970B

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PERL Program

; SEQ ID NO 106

; LENGTH: 4822

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1  
; NAME/KEY: unsure  
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-106

Query Match 62.1%; Score 2323.8; DB 4; Length 4822;  
Best Local Similarity 80.9%; Pred. No. 0;  
Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

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Qy      63 CGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTTCG 122
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      78 CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCG 137

Qy     123 GCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAAC 182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     138 GCTCAGT-----CGGCCCAGCCCCTCTCAGTCTTCCCCAACCCCCACAAC 182

Qy     183 CGCCCGCGACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     299 CACCCCGGCCGCGAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCCGAGGACGAGGAG- 357

Qy     362 ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC 421
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     358 --GAAGAAGAGGANGATGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGC 415

Qy     422 TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCG 475
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     416 TGGAGAGGAAGCCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCCAACGCCCTGCCGCCG 475

Qy     476 CCGCGCCGCTGTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGC 535
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     476 GCGCGCCNNTAATGGACTTCGGAAATGACTTCGTGCCGCCGCGCCCCGGGGACCCCTGC 535

Qy     536 CGGCCGCGCCCCCTGCCGCTCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG----- 589
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     536 CGGCCGCTCCCCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGT 595

Qy     590 ---CGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCAG 646
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     596 CGACCGTGCCCGCGCCATCCCCGCTGTCTGTGCGCGAGTCTCGCCCTCCAAGCTCCCTG 655

Qy     647 AGGACGACGAGCCTCCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGGAGCCCCCTGG 706
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     656 AGGACGACGAGCCTCCGGCCCCGCTCCCCCTCCTCCCCGCGCCAGCGTGAGCCCCCAGG 715
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|    |      |   |      |
|----|------|---|------|
| Qy | 707  | CGGAGC-----CCGCCGCGCCCCCTTCCACGCCGGCCG                        | 739  |
|    |      |   |      |
| Db | 716  | CAGAGCCCGTGTGGANCCCGCCAGCCCCGGCTNCCGCGCGCCCCCTCCACCCGGCCG     | 775  |
| Qy | 740  | CGCCCAAGCGCAGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTTCCTGCTG    | 796  |
|    |      |   |      |
| Db | 776  | CGCCCAAGCGCAGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTTCCTGCTG    | 835  |
| Qy | 797  | CATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAG  | 856  |
|    |      |   |      |
| Db | 836  | CATCTGAGCCTGTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAG   | 892  |
| Qy | 857  | GTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCT  | 916  |
|    |      |   |      |
| Db | 893  | GTAACACTATTTTCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCT | 952  |
| Qy | 917  | CTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGA   | 976  |
|    |      |   |      |
| Db | 953  | CTCTTCCTTCTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGA   | 1012 |
| Qy | 977  | ACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTA    | 1036 |
|    |      |   |      |
| Db | 1013 | ATTTGTCAACAGTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTA  | 1072 |
| Qy | 1037 | AAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAG  | 1096 |
|    |      |   |      |
| Db | 1073 | AAGAGGTCTCAGAGAAGGCAAAAACCTACTCATAGATAGAGATTTAACAGAGTTTTCAG   | 1132 |
| Qy | 1097 | AATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCA  | 1156 |
|    |      |   |      |
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| Qy | 1157 | TATTAGTAGAAAACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATT    | 1213 |
|    |      |   |      |
| Db | 1193 | TAATAGTAGCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGT  | 1252 |
| Qy | 1214 | TAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGG            | 1258 |
|    |      |   |      |
| Db | 1253 | TAGTTAGTAATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGG  | 1312 |
| Qy | 1259 | GTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGA  | 1318 |
|    |      |   |      |
| Db | 1313 | TTAAAGAGGATGAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAG   | 1372 |
| Qy | 1319 | TGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCAT  | 1378 |
|    |      |   |      |
| Db | 1373 | TTGCAGTGGAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTAT  | 1432 |
| Qy | 1379 | GGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----    | 1431 |
|    |      |   |      |
| Db | 1433 | GGGAAGTGAAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCG   | 1489 |
| Qy | 1432 | -----AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAA  | 1486 |
|    |      |   |      |
| Db | 1490 | AGAGCAACTTGGAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTA   | 1549 |
| Qy | 1487 | GTCTTGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCCAGAAC    | 1546 |



|    |      |   |      |
|----|------|---|------|
| Db | 1550 | ATCACGAAAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAG  | 1609 |
| Qy | 1547 | CTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCG  | 1603 |
| Db | 1610 | GTATAAAGGATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTG | 1669 |
| Qy | 1604 | AAAGCACCAAGCAAACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAG    | 1663 |
| Db | 1670 | AGAGCATTGCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCG  | 1729 |
| Qy | 1664 | ATG-AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCC  | 1719 |
| Db | 1730 | ATGAAAAAAAAAATAGAAGAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACC   | 1789 |
| Qy | 1720 | AAAACGTCAAATCC-TTTCCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAAC | 1778 |
| Db | 1790 | AAAACATCAAACCCTTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC  | 1849 |
| Qy | 1779 | AGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCC  | 1838 |
| Db | 1850 | AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC  | 1909 |
| Qy | 1839 | AGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGC | 1898 |
| Db | 1910 | AGATTTAGTACAGGAAGCATGTGAAAGTGAATGAATGAAGTTACTGGTACAAAGATTGC   | 1969 |
| Qy | 1899 | TTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAAGCTATACAAGAATCACTTTACCC | 1958 |
| Db | 1970 | TTATGAAACAAAATGGACTTGGTTCAAACATCAGAAAGTTATGCAAGAGTCACTCTATCC  | 2029 |
| Qy | 1959 | CACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGGCC  | 2018 |
| Db | 2030 | TGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGGCC  | 2089 |
| Qy | 2019 | TGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGT  | 2078 |
| Db | 2090 | TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGAT  | 2149 |
| Qy | 2079 | GCAGCCCAGTGATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCT   | 2138 |
| Db | 2150 | ACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACA  | 2206 |
| Qy | 2139 | TGAGCCTGAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTT   | 2195 |
| Db | 2207 | TGAGCCTGAAACCCCCCACCATATGAAGAGGCCATGAGTGATCACTAAAAAAGTATC     | 2266 |
| Qy | 2196 | GGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGA | 2255 |
| Db | 2267 | AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGA   | 2326 |
| Qy | 2256 | AGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCC  | 2315 |
| Db | 2327 | AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC  | 2386 |
| Qy | 2316 | AAGTCCAGATTTCTCTAATTATTAGAAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACA  | 2375 |

|    |      |  |      |
|----|------|--|------|
| Db | 2387 | AGCTCCGGATTTCCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCA | 2446 |
| Qy | 2376 | CGCTGAGCTAGTGGAGGATTCTCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGA  | 2435 |
|    |      |  |      |
| Db | 2447 | TTCTGAGCTAGTTGAAGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA  | 2506 |
| Qy | 2436 | TTCGATTCTTGAAGTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCT  | 2495 |
|    |      |  |      |
| Db | 2507 | TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT   | 2566 |
| Qy | 2496 | CACTGA-----AGTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTC     | 2549 |
|    |      |  |      |
| Db | 2567 | CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCCTT    | 2626 |
| Qy | 2550 | ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAA   | 2609 |
|    |      |  |      |
| Db | 2627 | GCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAA   | 2686 |
| Qy | 2610 | AGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAGGAGAAAATTTCTTTGCA    | 2666 |
|    |      |  |      |
| Db | 2687 | AGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAGGAGAAAATTCCTTTGCA    | 2746 |
| Qy | 2667 | AATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGA   | 2726 |
|    |      |  |      |
| Db | 2747 | GATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGC   | 2806 |
| Qy | 2727 | CAAAATAAAAGAAAGTGAAACATTTTCAGATTCTCTCCGATTGAGATAATAGATGAATT    | 2786 |
|    |      |  |      |
| Db | 2807 | ACAGATAAGAGAAACTGAAACGTTTTTCAGATTCTCTCCAATTGAAATTATAGATGAGTT   | 2866 |
| Qy | 2787 | TCCCACGTTTGTCTAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGA  | 2843 |
|    |      |  |      |
| Db | 2867 | CCCTACATTGATCAGTTCTAAAACTGATTCATTTCTAAATTAGCCAGGGAATATACTGA    | 2926 |
| Qy | 2844 | TCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCC  | 2903 |
|    |      |  |      |
| Db | 2927 | CCTAGAAGTATCCCAAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATTGCC   | 2986 |
| Qy | 2904 | TTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG----   | 2959 |
|    |      |  |      |
| Db | 2987 | TTGCACAGAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAA    | 3046 |
| Qy | 2960 | --TACATGTTTCAGATGAATTCTCCGAAAAATAGTCCAGTGTATCTAAGGCATCCATATC   | 3017 |
|    |      |  |      |
| Db | 3047 | AATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAGGTGCTCTTATT    | 3106 |
| Qy | 3018 | GCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAA   | 3077 |
|    |      |  |      |
| Db | 3107 | GCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAA   | 3166 |
| Qy | 3078 | ATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATC   | 3137 |
|    |      |  |      |
| Db | 3167 | AGTTCCTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATC   | 3226 |
| Qy | 3138 | CCTGTCAGCTGTATTGTCTGAGCAGAGCTGAG-TAAAACTTCAGTTGTTGACCTCCTCTACT | 3196 |
|    |      |  |      |
| Db | 3227 | ACCATCTGCTATATTTTCAGCAGAGCTGAGCTAAAACTTCAGTTGTTGACCTCCTGTACT   | 3286 |

Qy 3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC 3256  
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 Db 3287 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCAT 3346  
 Qy 3257 TGACAGTGTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGCCCTGCTCTCGGTGA 3316  
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 Db 3347 TGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGA 3406  
 Qy 3317 CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC 3376  
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 Db 3407 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC 3466  
 Qy 3377 ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT 3436  
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 Qy 3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCT 3496  
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 Qy 3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATG 3556  
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 Qy 3557 TTGGTGCCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616  
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 Qy 3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676  
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 Db 3707 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 3766  
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736  
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 Qy 3737 CAGA 3740  
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 Db 3827 CTGA 3830

# RESULT 2

US-08-700-607-2

; Sequence 2, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

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; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2

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Query Match 13.3%; Score 497.4; DB 2; Length 799;  
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Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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| Qy   | 3178 | GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTTTTGGTGCCAGC    | 3237 |
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| Qy   | 3238 | TTATTCCCTGCTGCTGTCTCTGACAGTGTTCAGCATTTGTCA GTGTAACGGCCTACATTGCC  | 3297 |
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| Db   | 228  | TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC     | 287  |
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| Qy   | 3358 | CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA     | 3417 |
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| Db   | 288  | CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT     | 347  |
| <br> |      |  |      |
| Qy   | 3418 | GAGGAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAA   | 3477 |
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| Db   | 348  | GAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG    | 407  |
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| Qy   | 3478 | GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA GTGTTG    | 3537 |
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| Db   | 408  | GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCA GTGTTG    | 467  |



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; EARLIER APPLICATION NUMBER: 60/047,588  
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; EARLIER APPLICATION NUMBER: 60/043,576
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; EARLIER APPLICATION NUMBER: 60/056,884
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; EARLIER APPLICATION NUMBER: 60/049,610
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Best Local Similarity 63.4%;  Pred. No. 2.5e-43;
Matches 350;  Conservative 0;  Mismatches 202;  Indels 0;  Gaps 0;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 3233
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| Qy | 3234 | CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTT    | CAGCATTGTCAGTGTAACGGCCTACAT                    | 3293 |
|    |      |                                       |  |      |
| Db | 346  | CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTT    | CAGTGTATCAGTGTGGTTTCTTACCT                     | 405  |
| Qy | 3294 | TGCCCTTGGCCCTGCTCTCGGTGACTATCAGCTTT   | AGGATATATAAGGGCGTGATCCAGGC                     | 3353 |
|    |      |                                       |  |      |
| Db | 406  | CATCCTGGCTCTTCTCTCTGTCAACATCAGCTTC    | AGGATCTACAAGTCCGTCATCCAAGC                     | 465  |
| Qy | 3354 | TATCCAGAAATCAGATGAAGGCCACCCATT        | CAGGGCATATTTAGAATCTGAAGTTGCTAT                 | 3413 |
|    |      |                                       |  |      |
| Db | 466  | TGTACAGAAGTCAGAAGAAGGCCATCCATT        | CAAAGCCTACCTGGACGTAGACATTACTCT                 | 525  |
| Qy | 3414 | ATCAGAGGAATTGGTTT                     | CAGAAATACAGTAATTTCTGCTCTTGGTCATGTGAACAGCACAAAT | 3473 |
|    |      |                                       |  |      |
| Db | 526  | GTCCTCAGAAGCTTTCCATAATTACATGAATGCT    | GCCATGGTGCACATCAACAGGGCCCT                     | 585  |
| Qy | 3474 | AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTT  | AGTTGATTCCCTGAAGTTTGCAGT                       | 3533 |
|    |      |                                       |  |      |
| Db | 586  | GAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCT  | GGTTGACTCCTTGAAGCTGGCTGT                       | 645  |
| Qy | 3534 | GTTGATGTGGGTGTTTACTTATGTTGGTGCCTT     | GTTCAATGGTCTGACACTACTGATTTT                    | 3593 |
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| Qy | 3594 | AGCTCTGATCTCACTCTTCAGTATTCTTGTTATTT   | TGAACGGCATCAGGTGCAGATAGA                       | 3653 |
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| Db | 706  | TGCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCT  | ATGAGAAGTACAAGACCCAGATTGA                      | 765  |
| Qy | 3654 | TCATTATCTAGGACTT                      | GCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA   | 3713 |
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| Db | 766  | TCACTATGTTGGCATCGCCCGAGATCAGACCAAGT   | CAATTGTTGAAAAGATCCAAGCAAA                      | 825  |
| Qy | 3714 | AATCCCTGGATT                          |  | 3725 |
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#### RESULT 4

US-09-149-476-255

; Sequence 255, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
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; EARLIER FILING DATE: 1997-10-02
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Matches 350;  Conservative 0;  Mismatches 202;  Indels 0;  Gaps 0;
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RESULT 5

US-08-700-607-4

; Sequence 4, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1095 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: THP1NOB01

; CLONE: 31870

US-08-700-607-4

Query Match 5.4%; Score 203.6; DB 2; Length 1095;

Best Local Similarity 61.6%; Pred. No. 1.3e-37;

Matches 337; Conservative 1; Mismatches 208; Indels 1; Gaps 1;

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# RESULT 6

US-09-149-476-102

; Sequence 102, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

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; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

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; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match 4.8%; Score 180.4; DB 4; Length 794;  
Best Local Similarity 61.0%; Pred. No. 2.6e-32;  
Matches 332; Conservative 6; Mismatches 202; Indels 4; Gaps 3;

```
Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTTGGTGTC 3233
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      253  TCGGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy      3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAACGGCC-TACA 3292
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      311  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCACTCARTGTGGGTTTCTTAMC 370

Qy      3293 TTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGG 3352
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      371  TCATCCTGGCTCTTCTCTCTGTCAACATCARCTTCAGGATCTACAAGTCCGTCAATCAAG 430

Qy      3353 CTATCCAGAAATCAGATGAAGGCCACCCATT-CAGGGCATATTTAGAATCTGAAGTTGCT 3411
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      431  CTGTWCAGAARTCAGAARAAGGCCATCCAWTCCAAAGCCTACCTGGACGTAGACATTACT 490

Qy      3412 ATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACA 3471
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      491  CTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCC 550

Qy      3472 ATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA 3531
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      551  CTGAAACTCATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 610

Qy      3532 GTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATT 3591
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      611  GTCTTCATGTGGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTTCTAATT 670

Qy      3592 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTATTTATGAACGGCATCAGGTGCAGATA 3651
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      671  CTTGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 730

Qy      3652 GATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCA 3711
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      731  GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGC 790

Qy      3712 AAAA 3715
          | | | |
Db      791 AAAA 794
```

RESULT 7  
US-08-700-607-9  
; Sequence 9, Application US/08700607

```

; Patent No. 5858708
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Goli, Surya K.
;   APPLICANT: Hillman, Jennifer L.
;   TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: U.S.
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/700,607
;     FILING DATE: Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 261 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     IMMEDIATE SOURCE:
;       LIBRARY: SPLNFET01
;       CLONE: 28742
US-08-700-607-9

```

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Query Match          4.4%;  Score 164.6;  DB 2;  Length 261;
Best Local Similarity 86.7%;  Pred. No. 6.7e-29;
Matches 176;  Conservative 0;  Mismatches 27;  Indels 0;  Gaps 0;

```

```

Qy      3237 CTTATTCCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTGAGTGTAAACGGCCTACATTGC 3296
          ||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1 CCTATNCCNGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGC 60

Qy      3297 CTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTAT 3356
          ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 CTTNGCCCTGCNCTCTGTGACCATCAGCTNTAGGCTATACAAGGGTGTGATCCAAGCTAT 120

Qy      3357 CCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATC 3416
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 CCAGAAATCAGATGAAGGNCACCCATTTCAGGGCATATCTGGANTCTGAAGTTGCTATATC 180

```

Qy 3417 AGAGGAATTGGTTCAGAAATACA 3439  
      ||||| ||| ||||| |||||  
Db 181 TGAGGAGTTGNTTCAGAAGTACA 203

RESULT 8

US-08-232-463-14/c

; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-Fls  
US-08-232-463-14

Query Match 2.0%; Score 75.4; DB 1; Length 7218;  
Best Local Similarity 5.3%; Pred. No. 1.8e-07;

Matches 22; Conservative 242; Mismatches 153; Indels 0; Gaps 0;

```

Qy      1127 TTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAA 1186
      ||||| | || | |:: : : : : : : : : : : : : : : : : :
Db      1459 TTAAAGAGATAGAAGAATTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1400

Qy      1187 TTGTGAGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAG 1246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1399 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1340

Qy      1247 AATCACCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTA 1306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1280

Qy      1307 ATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCAT 1366
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1220

Qy      1367 TTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTA 1426
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1160

Qy      1427 GAGCTAATGTGGAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAA 1486
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1159 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1100

Qy      1487 GTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAG 1543
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1043

```

# RESULT 9

US-09-128-155-16

; Sequence 16, Application US/09128155

; Patent No. 6117654

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/09/128,155

; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650

; EARLIER FILING DATE: 1998-07-02

; EARLIER APPLICATION NUMBER: US 60/054,646

; EARLIER FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 152331

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(152331)

; OTHER INFORMATION: n = A,T,C or G

US-09-128-155-16

Query Match 2.0%; Score 75.2; DB 3; Length 152331;  
Best Local Similarity 53.8%; Pred. No. 1e-06;  
Matches 155; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

|    |       |  |       |
|----|-------|--|-------|
| Qy | 463   | CCGCCCGCCGCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCC   | 522   |
|    |       |  |       |
| Db | 21936 | CCCCGCCCCCCCCGGCCCGCCCCCGCGCCCCCACCCCCCCCCCCCCCCCCCGCGCCC    | 21995 |
| Qy | 523   | CGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGC | 582   |
|    |       |  |       |
| Db | 21996 | CGCCCCCCCCCCCCGCGCCCCCAACCCCCCGCCCCCGCCCCCCCCCCCCCCCCACC     | 22055 |
| Qy | 583   | AGCCCCGCGGCGCCCGCGCCATCCCTGCCGCCCCTGCCGCGAGTCCTGCCCTCCAAGCTC | 642   |
|    |       |  |       |
| Db | 22056 | CCCCACACCCGGCCACACGCACCCCCACCCCGACGCCCCCGCCCCCCCCCCCCCGCAG   | 22115 |
| Qy | 643   | CCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCC  | 702   |
|    |       |  |       |
| Db | 22116 | CCGACGCCCCCCCCCGCCCGCCCGCCCCGCACCCCGACCCCCCGCCGCCCCGCCCC     | 22175 |
| Qy | 703   | CTGGCGGAGCCCGCCGCGCCCCCTTCCACGCGCGCCGCGCCCAAGCGC             | 750   |
|    |       |  |       |
| Db | 22176 | CCGCCCCCCCCCCCCCGGCCCCCCCCCGCCGGCGCGGGCGCCCCACCCC            | 22223 |

RESULT 10

US-09-894-998A-35/c

; Sequence 35, Application US/09894998A

; Patent No. 6537555

; GENERAL INFORMATION:

; APPLICANT: Hosken, Nancy Ann

; APPLICANT: Craig H. Day

; APPLICANT: Davin C. Dillon

; APPLICANT: McGowan, Patrick

; APPLICANT: Sleath, Paul R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

; FILE REFERENCE: 210121.538

; CURRENT APPLICATION NUMBER: US/09/894,998A

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 64

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 35

; LENGTH: 2481

; TYPE: DNA

; ORGANISM: HSV-2

US-09-894-998A-35

Query Match 2.0%; Score 74.6; DB 4; Length 2481;  
Best Local Similarity 48.7%; Pred. No. 1.6e-07;  
Matches 203; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 327 GTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGGAGGAGGACGAGGA 386  
| | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1920 GGACGCGGACGCGACGCTCCCACCAAGCCCCGCCGCAGAGGAAGAGGCGGAGGAGGAGGA 1861

Qy 387 GGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGCCCGCAGCCGGGCT 446  
 || ||| || ||||| ||||| ||||| | ||| | | | | |  
 Db 1860 GGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGAGGAGGAGGA 1801  
 Qy 447 GTCCGAGCTGCGGTGCCGCCCCCGCCCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTC 506  
 | | | | | | | | | | | | | | | | | | | | |  
 Db 1800 GGCGGAGGAGGAGGAGGCGGAGGAGGAGGAGGCGGCGGCGACCGCGGCCTGGGACGACGG 1741  
 Qy 507 GGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCA 566  
 | | | | | | | | | | | | | | | | | | | | |  
 Db 1740 AGACGCCGACGGGGCGCGGCGCCCGCGGACGCCGGGGCGAGCGGCCCGTGGCCGCGGTC 1681  
 Qy 567 GCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGCCCGCTGCCGCAGT 626  
 ||| | | | | | | | | | | | | | | | | | |  
 Db 1680 GCCCGAGTCCGAGTCCGGGGCCCGCGCGGCGCGCCCTCTTGGCCCCCACCCTGGGG 1621  
 Qy 627 CCTGCCCTCCAAGCTCCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCC 686  
 | | | | | | | | | | | | | | | | | | | | |  
 Db 1620 GGCGAGGGGCGAGCGCGGGGCGGCGGAGGAAGAGGCGGAGGACGAGGCCGCGGGGCCCGA 1561  
 Qy 687 AGCCGGCGCGAGCCCCCTGGCGGAGCCCGCGCGCCCCCTTCCACGCCGGCCGCGCC 743  
 ||| | | | | | | | | | | | | | | | | | |  
 Db 1560 GTCCGACCCGCGCCTCTTCCGGGGGCGGGCCCGCCCCCTCCGCGGCGTGGGGGGC 1504

# RESULT 11

US-09-103-840A-2/c

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; FEATURE:

; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 2.0%; Score 73.2; DB 3; Length 4403765;

Best Local Similarity 52.3%; Pred. No. 1.8e-05;

Matches 162; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 434 CCGCAGCCGGGCTGTCCGAGCTGCGGTGCCGCCCCCGCCCGCCGCGCCGCTGCTGGACT 493  
 ||| | | ||| |||| | ||| ||||| | | | ||||| | |



Db 3926346 CCGTGCCGGCGCTGCCCCGCGCCCGCGCCGCTTGGCCGCGCGGTGCCGCCGATAACCGG  
3926287

Qy 494 TCAGCAGCGACTCGGTGCCCCCGCGCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553

Db 3926286 CCTTGCCCGCGGCGCCGACAACCCCGCCGGTTCTTCCGGTGCCGGCGGCCCCGCGGCCG  
3926227

Qy 554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613

Db 3926226 CGCCGGCGCCGGCGTTACCGCCAGTCCCAACCGCGCCCGTCGGCGCCAATCCCGCTGG  
3926167

Qy 614 CCGCTGCCGCGAGTCTTGCCCTCCAAGCTCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673

Db 3926166 CATTATCAGCACCGGAGCCACCCATGCCGCCGCGCCGCTTGGCCGCGCGGTGCCGCCG  
3926107

Qy 674 CGCCTCCGCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCGCGCCCCCTTCCACGC 733

Db 3926106 CACCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCTGGCCGCCGACGCCG  
3926047

Qy 734 CGGCCGCGCC 743

Db 3926046 CGGCCCGGCC 3926037

## RESULT 12

US-09-103-840A-1/c

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 2.0%; Score 73.2; DB 3; Length 4411529;

Best Local Similarity 52.3%; Pred. No. 1.8e-05;

Matches 162; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCGCCGCTGCTGGACT 493

||| | | |||| |||| | ||| ||||| | | | ||||| | |

Db 3932558 CCGTGCCGGCGCTGCCCCGCGCCGCGGCGCCGCTTGGCCGCGGTGCCGCGGATAACCGG  
3932499

Qy 494 TCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGCGCGCGCCCCCTGCCG 553  
| | | | | | | | | | | | | | | | | | | | | |

Db 3932498 CCTTGCCCCGCGGCGCCGACAACCCCGCCGGTTCTCCGGTGCCGCGGCCCCCGCGGCCC  
3932439

Qy 554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613  
| | | | | | | | | | | | | | | | | | | | | |

Db 3932438 CGCCGGCGCGGCGTTACCGCCAGTCCCACCGCGCCGCGTCGGCGCCAATCCCGCTGG  
3932379

Qy 614 CCGTGCCGCGATCCTGCCCTCCAAGCTCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673  
| | | | | | | | | | | | | | | | | | | | | |

Db 3932378 CATTATCAGCACCGGAGCCACCCATGCCGCGGCGCCGCTTGCGCGCCGGTGCCGCGG  
3932319

Qy 674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCGCGCCCCCTTCCACGC 733  
| | | | | | | | | | | | | | | | | | | | | |

Db 3932318 CACCACCGGAGCCGTTGATGCCGCGGCAATGGCGTTGCCGCGCCTGGCCGCGGACGCCCG  
3932259

Qy 734 CGGCCGCGCC 743  
| | | | | | | |

Db 3932258 CGGCCCGGCC 3932249

# RESULT 13

US-09-165-264-8/c

; Sequence 8, Application US/09165264

; Patent No. 6197510

; GENERAL INFORMATION:

; APPLICANT: Vinayagamoorthy, Thuraiayah

; TITLE OF INVENTION: Multi-Loci Genomic Analysis

; FILE REFERENCE: 44747

; CURRENT APPLICATION NUMBER: US/09/165,264

; CURRENT FILING DATE: 1998-10-01

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 319

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence

US-09-165-264-8

Query Match 1.8%; Score 68.6; DB 3; Length 319;

Best Local Similarity 52.2%; Pred. No. 1.3e-06;

Matches 152; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy 454 GCTGCGGTGCCGCCCCGCCGCCGCGCGCTGCTGGACTTCAGCAGCGACTCGGTGCCC 513  
| | | | | | | | | | | | | | | | | | | | | |

Db 308 GCTGCAGACC 249

Qy 514 CCCGCGCCCCGCGGGCCGCTGCCGCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCC 573

[illegible]

Query Match 1.8%; Score 68; DB 3; Length 4403765;  
Best Local Similarity 48.9%; Pred. No. 0.00029;  
Matches 216; Conservative 0; Mismatches 220; Indels 6; Gaps 1;

Db 3925823 GGGTGTCTCGGTGGCACTGGTGGTAAGGGCGGTGTCTGGCGGCGTGGCTGGCCTCGGCGGGGC 3925882  
 Qy 482 CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCG 541  
 Db 3925883 CGGTGGTGCCTCGGGCCAGCTCTTCAGCGCCGGAGGCGCGGCGGGTGCCGTTGGGGTTGG 3925942  
 Qy 542 CGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGC 601  
 Db 3925943 CGGCACCGGCGGCCAGGGTGGGGCTGGCGGTGCCGGAGCGGCCGGCGCCGACGCCCCCGC 3926002  
 Qy 602 CATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTC 661  
 Db 3926003 CAGCACAG-----GTCTAACCGGTGGTACCGGGTTCTGCTGGCGGGGCCGGCGGCGTCTGG 3926056  
 Qy 662 CGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGC 721  
 Db 3926057 CGGCCAGGGCGGCAACGCCATTGCCGGCGGCATCAACGGCTCCGGTGGTGCCGGCGGCAC 3926116  
 Qy 722 CCCCTTCCACGCCGGCCGCGCC 743  
 Db 3926117 CGGCGGCCAAGGCGGCGCCGGC 3926138

Db 3931915 CCGCGCCGGTGGCGCCGGCGGTTCGCGGCGCACTGCTGCTGGGCGCTGGCGGACAGGGCGG 3931974  
 Qy 362 ACGAGGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC 421  
 Db 3931975 CCTCGGCGGCGCCGGCGGACAAGGCGGCACCGGCGGGGCCGGCGGAGATGGCGTTCTGGG 3932034  
 Qy 422 TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCGAGCTGCGGTGCCGCCCCGCCGCCGCCGCGC 481  
 Db 3932035 GGGTGTTCGGTGGCACTGGTGGTAAGGGCGGTGTTCGGCGGCGTGGCTGGCCTCGGCGGGGC 3932094  
 Qy 482 CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCG 541  
 Db 3932095 CGGTGGTGCCCGGGCCAGCTCTTCAGCGCCGAGGCGCGGCGGTGCCGTGGGGTTGG 3932154  
 Qy 542 CGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCCGGGCGCCCCGCGC 601  
 Db 3932155 CGGCACCGGCGGCCAGGGTGGGGCTGGCGGTGCCGAGCGGCCGGCGCCGACGCCCCCGC 3932214  
 Qy 602 CATCCCTGCCGCCCCTGCGCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTC 661  
 Db 3932215 CAGCACAG-----GTCTAACCGGTGGTACCGGGTTCGCTGGCGGGGCCGGCGGCGTCCG 3932268  
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Job time : 202.668 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:28:33 ; Search time 1125.66 Seconds  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2  | 2343.6 | 62.6  | 4053 | 9  | US-09-758-140-5     | Sequence 5, Appli   |
| 3  | 2343.6 | 62.6  | 4053 | 9  | US-09-972-599A-5    | Sequence 5, Appli   |
| 4  | 2343.6 | 62.6  | 4632 | 15 | US-10-060-036-53    | Sequence 53, Appl   |
| 5  | 2289.2 | 61.2  | 3579 | 9  | US-09-789-386-1     | Sequence 1, Appli   |
| 6  | 2289.2 | 61.2  | 3579 | 9  | US-09-893-348-22    | Sequence 22, Appl   |
| 7  | 1088.8 | 29.1  | 1980 | 13 | US-10-220-891-22    | Sequence 22, Appl   |
| 8  | 809.8  | 21.6  | 2782 | 13 | US-10-205-194-165   | Sequence 165, App   |
| 9  | 497.4  | 13.3  | 1122 | 9  | US-09-789-386-5     | Sequence 5, Appli   |
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| 11 | 497.4  | 13.3  | 1785 | 12 | US-10-439-388-62    | Sequence 62, Appl   |
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| 13 | 495.8  | 13.3  | 1610 | 9  | US-09-765-205-5     | Sequence 5, Appli   |
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| 17 | 322.4  | 8.6   | 389  | 10 | US-09-960-352-5154  | Sequence 5154, Ap   |
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| 19 | 266.4  | 7.1   | 668  | 12 | US-10-264-237-163   | Sequence 163, App   |
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| 21 | 253.2  | 6.8   | 3202 | 10 | US-09-954-456-210   | Sequence 210, App   |
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| 23 | 244.4  | 6.5   | 1502 | 13 | US-10-205-219-94    | Sequence 94, Appl   |
| 24 | 242.4  | 6.5   | 1473 | 13 | US-10-205-194-128   | Sequence 128, App   |
| 25 | 231.8  | 6.2   | 3637 | 12 | US-10-108-260A-449  | Sequence 449, App   |
| 26 | 231.8  | 6.2   | 3637 | 12 | US-10-159-563-443   | Sequence 443, App   |
| 27 | 228.8  | 6.1   | 1330 | 15 | US-10-106-698-1945  | Sequence 1945, Ap   |
| 28 | 228.8  | 6.1   | 1656 | 9  | US-09-729-674-19    | Sequence 19, Appl   |
| 29 | 228.8  | 6.1   | 1668 | 9  | US-09-765-205-25    | Sequence 25, Appl   |
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| 33 | 228.8  | 6.1   | 2664 | 13 | US-09-882-171-255   | Sequence 255, App   |
| 34 | 194.4  | 5.2   | 489  | 11 | US-09-918-995-15830 | Sequence 15830, A   |
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| 36 | 180.4  | 4.8   | 794  | 11 | US-09-809-391-102   | Sequence 102, App   |
| 37 | 180.4  | 4.8   | 794  | 13 | US-09-882-171-102   | Sequence 102, App   |
| 38 | 174    | 4.7   | 198  | 9  | US-09-758-140-19    | Sequence 19, Appl   |
| 39 | 174    | 4.7   | 198  | 9  | US-09-972-599A-19   | Sequence 19, Appl   |
| 40 | 174    | 4.7   | 198  | 9  | US-09-972-599A-21   | Sequence 21, Appl   |
| 41 | 170.2  | 4.5   | 3413 | 14 | *p2125X001-843-61   | Sequence 843, Appl7 |
| 42 | 153.4  | 4.1   | 330  | 14 | US-10-040-739-366   | Sequence 366, App   |
| 43 | 134.4  | 3.6   | 573  | 13 | US-10-101-510-401   | Sequence 401, App   |
| 44 | 132.8  | 3.5   | 259  | 10 | US-09-960-352-13803 | Sequence 13803, A   |
| 45 | 126.8  | 3.4   | 406  | 10 | US-09-960-352-2239  | Sequence 2239, Ap   |

#### ALIGNMENTS

#### RESULT 1

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

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; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17

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Query Match          100.0%; Score 3739.4; DB 9; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG 60

Qy     61 ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120
        |||
Db     61 ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT 120

Qy    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180
        |||
Db    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCA¢ 180

Qy    181 ACCGCCC GCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
        |||
Db    181 ACCGCCC GCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
        |||
Db    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300

Qy    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
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Db    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360

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|    |      |   |      |
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| Qy | 361  | GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG  | 420  |
|    |      |   |      |
| Db | 361  | GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG  | 420  |
| Qy | 421  | CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG  | 480  |
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| Db | 421  | CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG  | 480  |
| Qy | 481  | CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC   | 540  |
|    |      |   |      |
| Db | 481  | CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC   | 540  |
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| Qy | 601  | CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT  | 660  |
|    |      |   |      |
| Db | 601  | CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT  | 660  |
| Qy | 661  | CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG  | 720  |
|    |      |   |      |
| Db | 661  | CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG  | 720  |
| Qy | 721  | CCCCCTTCCACGCCGGCCGCGCCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT | 780  |
|    |      |   |      |
| Db | 721  | CCCCCTTCCACGCCGGCCGCGCCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT | 780  |
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|    | 781  | TTTGCTCTCCTGCTGCATCTGAGCCTGTGATAACCTCCTCTGCAGAAAAAATTATGGAT   | 840  |
| Qy | 841  | TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG  | 900  |
|    |      |   |      |
| Db | 841  | TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG  | 900  |
| Qy | 901  | CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTAAAGAA   | 960  |
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| Db | 901  | CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTAAAGAA   | 960  |
| Qy | 961  | CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACT    | 1020 |
|    |      |   |      |
| Db | 961  | CATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACT    | 1020 |
| Qy | 1021 | TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT  | 1080 |
|    |      |   |      |
| Db | 1021 | TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT  | 1080 |
| Qy | 1081 | TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA   | 1140 |
|    |      |   |      |
| Db | 1081 | TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA   | 1140 |
| Qy | 1141 | AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA | 1200 |
|    |      |   |      |
| Db | 1141 | AAAGGAGAGTCAGCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA | 1200 |
| Qy | 1201 | GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT  | 1260 |

|    |      |  |      |
|----|------|--|------|
| Db | 1201 | <br>GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT | 1260 |
| Qy | 1261 | AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATG    | 1320 |
| Db | 1261 | AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATG    | 1320 |
| Qy | 1321 | TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG     | 1380 |
| Db | 1321 | TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG     | 1380 |
| Qy | 1381 | GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA     | 1440 |
| Db | 1381 | GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA     | 1440 |
| Qy | 1441 | ACAGAAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT               | 1500 |
| Db | 1441 | AGTAAAGTGGACAGAAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT     | 1500 |
| Qy | 1501 | AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGC      | 1560 |
| Db | 1501 | AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGC      | 1560 |
| Qy | 1561 | TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC     | 1620 |
| Db | 1561 | TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC     | 1620 |
| Qy | 1621 | ACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAATAGAA     | 1680 |
| Db | 1621 | ACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAACCTAGAA     | 1680 |
| Qy | 1681 | GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCCTT    | 1740 |
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| Db | 1741 | GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT     | 1800 |
| Qy | 1801 | GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGAAGCATGT    | 1860 |
| Db | 1801 | GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGAAGCATGT    | 1860 |
| Qy | 1861 | GAAAGTGAACCTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG    | 1920 |
| Db | 1861 | GAAAGTGAACCTGAATGAAGCCACATTTACAAAGATTGCTTATGAAACAAAAGTGGACTTG    | 1920 |
| Qy | 1921 | GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA      | 1980 |
| Db | 1921 | GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA      | 1980 |
| Qy | 1981 | TTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCACCA     | 2040 |
| Db | 1981 | TTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATGGAAGCACCA     | 2040 |
| Qy | 2041 | TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTATCCCCACTG      | 2100 |

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|----|------|---|-------|
| Db | 2041 | TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG    | 2100  |
| Qy | 2101 | GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA     | 2160  |
|    |      |   |       |
| Db | 2101 | GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA     | 2160  |
| Qy | 2161 | TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG    | 2220  |
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| Db | 2161 | TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG    | 2220  |
| Qy | 2221 | CCTGAAAGTTTTAATGCAGCTGTTTCAAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT  | 2280  |
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| Db | 2221 | CCTGAAAGTTTTAATGCAGCTGTTTCAAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT  | 2280  |
| Qy | 2281 | GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA    | 2340  |
|    |      |   | 12430 |
| Db | 2281 | GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA    | 2340  |
| Qy | 2341 | GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCA    | 2400  |
|    |      |   |       |
| Db | 2341 | GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCA    | 2400  |
| Qy | 2401 | CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACA   | 2460  |
|    |      |   |       |
| Db | 2401 | CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACA   | 2460  |
| Qy | 2461 | CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC    | 2520  |
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| Db | 2461 | CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC    | 2520  |
| Qy | 2521 | CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAA                  | 2580  |
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| Db | 2521 | CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG    | 2580  |
| Qy | 2581 | TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG    | 2640  |
|    |      |   |       |
| Db | 2581 | TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG    | 2640  |
| Qy | 2641 | ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTAATACTGCAATTTATTCAAAT    | 2700  |
|    |      |   |       |
| Db | 2641 | ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTAATACTGCAATTTATTCAAAT    | 2700  |
| Qy | 2701 | GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA    | 2760  |
|    |      |   |       |
| Db | 2701 | GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA    | 2760  |
| Qy | 2761 | TCTCCGATTGAGATAAATAGATGAATTTCCCACGTTTGTGTCAGTGCTAAAGATGATTCTCCT | 2820  |
|    |      |   |       |
| Db | 2761 | TCTCCGATTGAGATAAATAGATGAATTTCCCACGTTTGTGTCAGTGCTAAAGATGATTCTCCT | 2820  |
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|    |      |   |       |
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|    |      |  |      |
| Db | 2941 | ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA   | 3000 |
| Qy | 3001 | TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC   | 3060 |
|    |      |  |      |
| Db | 3001 | TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC   | 3060 |
| Qy | 3061 | AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA   | 3120 |
|    |      |  |      |
| Db | 3061 | AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA   | 3120 |
| Qy | 3121 | GAGAAAGAGGACAGATCCCTGTGCTGCTGATTGTGTCAGCAGAGCTGAGTAAACCTTCAGTT | 3180 |
|    |      |  |      |
| Db | 3121 | GAGAAAGAGGACAGATCCCTGTGCTGCTGATTGTGTCAGCAGAGCTGAGTAAACCTTCAGTT | 3180 |
| Qy | 3181 | GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCCAGCTTA     | 3240 |
|    |      |  |      |
| Db | 3181 | GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCCAGCTTA     | 3240 |
| Qy | 3241 | TTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGTCAGTGTAACGGCCTACATTGCCTTG | 3300 |
|    |      |  |      |
| Db | 3241 | TTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGTCAGTGTAACGGCCTACATTGCCTTG | 3300 |
| Qy | 3301 | GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG   | 3360 |
|    |      |  |      |
| Db | 3301 | GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG   | 3360 |
| Qy | 3361 | AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG  | 3420 |
|    |      |  |      |
| Db | 3361 | AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG  | 3420 |
| Qy | 3421 | GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA  | 3480 |
|    |      |  |      |
| Db | 3421 | GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA  | 3480 |
| Qy | 3481 | CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTGATG    | 3540 |
|    |      |  |      |
| Db | 3481 | CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTGATG    | 3540 |
| Qy | 3541 | TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG   | 3600 |
|    |      |  |      |
| Db | 3541 | TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG   | 3600 |
| Qy | 3601 | ATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT  | 3660 |
|    |      | 075X2  | 385  |
| Db | 3601 | ATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT  | 3660 |
| Qy | 3661 | CTAGGACTTGCAAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT  | 3720 |
|    |      |  |      |
| Db | 3661 | CTAGGACTTGCAAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT  | 3720 |
| Qy | 3721 | GGATTGAAGCGCAAAGCAGAT  | 3741 |
|    |      |  |      |
| Db | 3721 | GGATTGAAGCGCAAAGCAGAT  | 3741 |

US-09-758-140-5

Query Match 62.6%; Score 2343.6; DB 9; Length 4053;  
Best Local Similarity 81.3%; Pred. No. 0;  
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 134 | CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACC GCCCGCGC ACT | 193 |
|    |     |  |     |
| Db | 16  | CTCGGCTCAGTCGGCCCAGCCCCCTCTCAGTCCTCCCCAACCCCCACAACC GCCCGCGG CT  | 75  |
| Qy | 194 | CTGAGGAGAAGCGGC - CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC   | 252 |
|    |     |  |     |
| Db | 76  | CTGAGACGCGGCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC - TCCACCCTCCAGCC    | 134 |
| Qy | 253 | ATGGAAGACATAGACCAGTCGTGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCT       | 312 |
|    |     | A C T T G C T  |     |
| Db | 135 | ATGGAAGACCTGGACCAGTCTCCTCTGGT --- CTCGTCTCGGACAGCCCACCCG GCG     | 191 |
| Qy | 313 | CCGCCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG    | 372 |
|    |     |  |     |
| Db | 192 | CAGCCCGCGCTTCAAGTACCAGTTTCGTGAGGGAGCCCGAGGACGAGGAG --- GAAGAAGAG | 248 |
| Qy | 373 | GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG     | 432 |
|    |     |  |     |
| Db | 249 | GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG     | 308 |
| Qy | 433 | CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC ----- CGCCCGCCGCCCGCGCGCGCTG     | 486 |



Db 1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329  
 ||||| ||||| ||| ||||| ||||| ||| ||||| |||

Db 1206 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA 1265

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389  
 || ||| ||||| || ||||| ||||| || ||||| ||| ||||| |||||

Db 1266 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1325

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437  
 |||| | ||| | ||| ||| || ||||| ||||| ||| || |||

Db 1326 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTG 1382

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497  
 ||||| ||||| || ||||| || ||||| ||||| ||||| urφmφcu|d0||

Db 1383 GAAAGTAAAGTGGATAAAAAATGTTTTCAGATAGCCTTGAGCAAACATAACGAAAAA 1442

Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557  
 ||||| || || ||||| || ||||| ||||| ||||| ||||| || |||||

Db 1443 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1502

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614  
 | || ||||| || ||||| || ||||| || ||||| || ||||| ||

Db 1503 CGTTCAGGAGCATATATCATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA 1562

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674  
 ||||| ||| ||||| ||||| ||||| ||||| ||||| || ||||| |||||

Db 1563 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1622

Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG- ACTAGCCCCAAACGTCAAAT 1731  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1623 ATAGAAGAAAAGGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC 1682

Qy 1732 CCTTTCCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1683 CCTTTTCTTGTTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1742

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851  
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Db 1743 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1802

Qy 1852 GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911  
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Db 1803 GAAGCATGTGAAAGTGAAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1862

Qy 1912 GTGGA TCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971  
 ||||| ||||| ||||| ||||| ||| ||||| ||||| || ||| ||||| |||||

Db 1863 ATGGACTTGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1922

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTGCCTGATATTGTTATG 2031  
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1923 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTGCCTGACATTGTTATG 1982

Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA 2091  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1983 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA 2042

|    |      |   |      |
|----|------|---|------|
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGCACAGTATAAAAGCTTGAGCCTGAAAAAC | 2151 |
| Db | 2043 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAAC   | 2099 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGAACAAAGGAA     | 2208 |
| Db | 2100 | CCCCCACCATATGAAGAGGCCATGAGTGTATCTACTAAAAAAAGTATCAGGAATAAAGGAA   | 2159 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA   | 2268 |
| Db | 2160 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA    | 2219 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC   | 2328 |
| Db | 2220 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGATTTTC    | 2279 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG   | 2388 |
| Db | 2280 | TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT   | 2339 |
| Qy | 2389 | GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTCCTGAA     | 2448 |
| Db | 2340 | GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC    | 2399 |
| Qy | 2449 | GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A      | 2502 |
| Db | 2400 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA    | 2459 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA    | 2562 |
| Db | 2460 | TTTGAGTCAATGATAGAAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA   | 2519 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA    | 2619 |
| Db | 2520 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA     | 2579 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT   | 2679 |
| Db | 2580 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC   | 2639 |
| Qy | 2680 | AATAC'TGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA   | 2739 |
| Db | 2640 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA    | 2699 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC    | 2799 |
| Db | 2700 | ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC   | 2759 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC    | 2856 |
| Db | 2760 | AGTTCTAAAAC'TGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC  | 2819 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG   | 2916 |
| Db | 2820 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAATTG     | 2879 |



|    |      |  |      |
|----|------|--|------|
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA    | 2970 |
|    |      |  |      |
| Db | 2880 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA   | 2939 |
| Qy | 2971 | GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC   | 3030 |
|    |      |  |      |
| Db | 2940 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT   | 2999 |
| Qy | 3031 | TCTGCTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA    | 3090 |
|    |      |  |      |
| Db | 3000 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA   | 3059 |
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCTAGCTGTA  | 3150 |
|    |      |  |      |
| Db | 3060 | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA   | 3119 |
| Qy | 3151 | TTGTCTGAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG    | 3210 |
|    |      |  |      |
| Db | 3120 | TTTTCTGAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG    | 3179 |
| Qy | 3211 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTCAGC   | 3270 |
|    |      |  |      |
| Db | 3180 | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTTTTCATTGACAGTATTTCAGC | 3239 |
| Qy | 3271 | ATTGTCTAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG  | 3330 |
|    |      |  |      |
| Db | 3240 | ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG   | 3299 |
| Qy | 3331 | ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3390 |
|    |      |  |      |
| Db | 3300 | ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA  | 3359 |
| Qy | 3391 | TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT   | 3450 |
|    |      |  |      |
| Db | 3360 | TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAATACAGTAATTCTGCT   | 3419 |
| Qy | 3451 | CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA   | 3510 |
|    |      |  |      |
| Db | 3420 | CTTGGTCATGTGAACCTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA  | 3479 |
| Qy | 3511 | GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT    | 3570 |
|    |      |  |      |
| Db | 3480 | GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT    | 3539 |
| Qy | 3571 | AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCTGTTATTTAT    | 3630 |
|    |      |  |      |
| Db | 3540 | AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT   | 3599 |
| Qy | 3631 | GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT   | 3690 |
|    |      |  |      |
| Db | 3600 | GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT   | 3659 |
| Qy | 3691 | GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA             | 3740 |
|    |      |  |      |
| Db | 3660 | GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA             | 3709 |

RESULT 3

US-09-972-599A-5

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; Sequence 5, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein
(KIAA0886, GenBank
; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)
US-09-972-599A-5
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Query Match          62.6%; Score 2343.6; DB 9; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;
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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      16 CTCGGCTCAGTCGGCCAGCCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 CTGAGACGCGGCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCCTCCAGCC 134
      3 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTAGGAGATGGAGAGCCCCGCCCGGCGCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTCAAGTACCAGTTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAG 432
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308
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|    |      |                                  |                                  |      |
|----|------|----------------------------------|----------------------------------|------|
| Qy | 433  | CCCCGAGCCCGGGCTGTCCGCGAGTGC      | CGGTGC-----CGCCCGCCGCCGCCCGCCCTG | 486  |
|    |      |                                  |                                  |      |
| Db | 309  | CCCCGCCCGGGCTGTCCGCGGCCCCAGTGCC  | ACCGCCCCTGCCGCCGGCGCGCCCCCTG     | 368  |
| Qy | 487  | CTGGACTTCAGCAGCGACTCGGTGCCCCCGCG | CCCCCGGGCCGCTGCCGGCCGCGCCC       | 546  |
|    |      |                                  |                                  |      |
| Db | 369  | ATGGACTTCGGAATGACTTCGTGCCGCCGGCG | CCCCCGGGGACCCCTGCCGCCGCGTCCC     | 428  |
| Qy | 547  | CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGA | ACGCAGCCCCG-----CGGCGCCC         | 597  |
|    |      |                                  |                                  |      |
| Db | 429  | CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGG  | ACCCGAGCCCGGTGTCTGTCGACCGTGCCC   | 488  |
| Qy | 598  | GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCT | GCCCTCCAAGCTCCCAGAGGACGACGAG     | 657  |
|    |      |                                  |                                  |      |
| Db | 489  | GCGCCATCCCCGCTGTCTGCTGCCGCAGTCT  | GCCCTCCAAGCTCCCTGAGGACGACGAG     | 548  |
| Qy | 658  | CCTCCGCGCAGGCCCCCGCCTCCGCCGCCAGC | CGGCGCAGCCCCCTGGCGGAG-----       | 711  |
|    |      |                                  |                                  |      |
| Db | 549  | CCTCCGCCCCGGCCTCCCCCTCCTCCCCCGGC | CAGCGTGAGCCCCCAGGCAGAGCCCGTG     | 608  |
| Qy | 712  | -----CCCCGCCGCCCCCTTCCACGCCGGC   | CGCCGCCCCAAGCGC                  | 750  |
|    |      |                                  |                                  |      |
| Db | 609  | TGGACCCCGCCAGCCCCGGCTCCCGCCGCGC  | CCCCCTCCACCCCGGCCGCCCCAAGCGC     | 668  |
| Qy | 751  | AGGGGCTCC---GGCTCAGTGATGAGACCCTT | TTTGCTCTTCTCTGCTGCATCTGAGCCT     | 807  |
|    |      |                                  |                                  |      |
| Db | 669  | AGGGGCTCCTCGGGCTCAGTGATGAGACCCTT | TTTGCTCTTCTCTGCTGCATCTGAGCCT     | 728  |
| Qy | 808  | GTGATACCCTCCTCTGCAGAAAAATTATGGAT | TTTGATGGAGCAGCCAGGTAACTGTT       | 867  |
|    |      |                                  |                                  |      |
| Db | 729  | GTGATACGCTCCTCTGCAGAAAA--TATGGAC | TGTAAGGAGCAGCCAGGTAACTATT        | 785  |
| Qy | 868  | TCGTCTGGTCAAGAGGATTTCCCATCTGTCT  | GCTTGAACTGCTGCCTCTCTTCCTTCT      | 927  |
|    |      |                                  |                                  |      |
| Db | 786  | TCGGCTGGTCAAGAGGATTTCCCATCTGTCT  | GCTTGAACTGCTGCCTCTCTTCCTTCT      | 845  |
| Qy | 928  | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGA | CATGGATACCTTGGTAACTTATCAGCA      | 987  |
|    |      |                                  |                                  |      |
| Db | 846  | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGA | CATGAATACCTTGGTAATTTGTCAACA      | 905  |
| Qy | 988  | GTGTCATCCTCAGAAGGAACAATTGAAGAACT | TTTAAATGAAGCTTCTAAAGAGTTGCCA     | 1047 |
|    |      |                                  |                                  |      |
| Db | 906  | GTATTACCCACTGAAGGAACACTTCAAGAAAA | TGTCAGTGAAGCTTCTAAAGAGGTCTCA     | 965  |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGA | TTTAGCAGAATTTTCAGAATTAGAATAT     | 1107 |
|    |      |                                  |                                  |      |
| Db | 966  | GAGAAGGCAAAAACTCTACTCATAGATAGAGA | TTTAAACAGAGTTTTCAGAATTAGAATAC    | 1025 |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCC  | CAAAAGGAGAGTCAGCCATATTAGTAGAA    | 1167 |
|    |      |                                  |                                  |      |
| Db | 1026 | TCAGAAATGGGATCATCGTTCAGTGTCTCTC  | CAAAAGCAGAATCTGCCGTAATAGTAGCA    | 1085 |
| Qy | 1168 | AACAC'TAAGGAAGAAGTAATTGTGAGGAGTA | AAA---GACAAAGAGGATTTAGTTGTAGT    | 1224 |
|    |      |                                  |                                  |      |
| Db | 1086 | AATCCTAGGGAAGAAATAATCGTGAAAAATA  | AAAGATGAAGAAGAGAAGTTAGTTAGTAAT   | 1145 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAAGAGAC            | 1269 |
| Db | 1146 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT  | 1205 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA  | 1329 |
| Db | 1206 | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA   | 1265 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA  | 1389 |
| Db | 1266 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA  | 1325 |
| Qy | 1390 | GATAC TTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG        | 1437 |
| Db | 1326 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG  | 1382 |
| Qy | 1438 | GAAAGTAAAGTGAGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG  | 1497 |
| Db | 1383 | GAAAGTAAAGTGAGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA  | 1442 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCCAGAACCTGTGAAGGAC   | 1557 |
| Db | 1443 | GATAGTGAGAGTAGTAATGATGATAC TCTTTCCCAGTACGCCAGAAGGTATAAAGGAT   | 1502 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA  | 1614 |
| Db | 1503 | CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA  | 1562 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTTGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA   | 1674 |
| Db | 1563 | ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA   | 1622 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAACGTCAAAT   | 1731 |
| Db | 1623 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC   | 1682 |
| Qy | 1732 | CCTTTCCTTG TAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA | 1791 |
| Db | 1683 | CCTTTCCTTG TAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTAACA   | 1742 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG  | 1851 |
| Db | 1743 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG  | 1802 |
| Qy | 1852 | GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA  | 1911 |
| Db | 1803 | GAAGCATGTGAAAGTGAAATGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA  | 1862 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT   | 1971 |
| Db | 1863 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT  | 1922 |
| Qy | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTACCAGTTTTGCCTGATATTGTTATG   | 2031 |
| Db | 1923 | TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG  | 1982 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA  | 2091 |

|    |      |  |      |
|----|------|--|------|
| Db | 1983 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA   | 2042 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC   | 2151 |
| Db | 2043 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC   | 2099 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA   | 2208 |
| Db | 2100 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA   | 2159 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA  | 2268 |
| Db | 2160 | GAAATTAAAGAGCCTGAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA    | 2219 |
| Qy | s    | TTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTGGAATG   | 2228 |
| Db | 2220 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTC   | 2279 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG  | 2388 |
| Db | 2280 | TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT  | 2339 |
| Qy | 2389 | GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCCGATTCCTGAA | 2448 |
| Db | 2340 | GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC  | 2399 |
| Qy | 2449 | GTCCCACAAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A   | 2502 |
| Db | 2400 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTC lyp CTGA, 2459  | 2459 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA   | 2562 |
| Db | 2460 | TTTGAGTCAATGATAGAATATGAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA     | 2519 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA   | 2619 |
| Db | 2520 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA   | 2579 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT  | 2679 |
| Db | 2580 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC  | 2639 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA   | 2739 |
| Db | 2640 | AGTACTGCAGTTT ATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA           | 2699 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC  | 2799 |
| Db | 2700 | ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC  | 2759 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC   | 2856 |
| Db | 2760 | AGTTCTAAACTGATTCAATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC   | 2819 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG   | 2916 |

Db 2820 CACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTTCATTGCCTTGACAGAAATTG 2879

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970  
 ||| ||||| ||||| ||||| ||| | || ||||| ||||| | ||| |||

Db 2880 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2939

Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030  
 ||||| ||| || ||||| ||||| | ||| ||||| ||||| |||||

Db 2940 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2999

Qy 3031 TCTGCTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090  
 ||||| ||||| ||||| ||| | ||||| ||||| ||||| ||||| |||||

Db 3000 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 3059

Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150  
 ||||| ||||| ||||| ||||| ||| ||||| ||||| ||||| ||||| |||||

Db 3060 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3119

Qy 3151 TTGTGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3120 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3179

Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC 3270  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3180 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC 3239

Qy 3271 ATTGTGAGTGAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330  
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3240 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3299

Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3300 ATATACAAGGCTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3359

Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450  
 ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3360 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3419

Qy 3451 CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3420 CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3479

Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3480 GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3539

Qy 3571 AATGGTCTGACAC TAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3540 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3599

Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3600 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3659

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740  
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

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; GENERAL INFORMATION:

APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

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Best Local Similarity 81.3%; Pred. No. 0;  
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

QY 134 CACGACTCGGCCTGCGCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT 193

Db 23 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 82

Qy 194 CTGAGGAGAAGCGGC-CTTGGCGGCGGCTGTAGCTGCAGCATCGTTCGGCGACCCGCCAGCC 252

Db 83 CTGAGACGCGGCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 141

QY 253 ATGGAAGACATAGACCAAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCGCCCGGCCT 312

Db 142 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCCACCCCGGCCG 198

Qy 313 CCGCCCGCCTTCAAGTACCAAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372

Db 199 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 255

QY 373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAC TGGAGGTGCTGGAGAGGAAG 432

Db 256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315

QY 433 CCCGAGCCGGGCTGTCCGAGCTGCGGTGC-----CGCCCGCCGCCGCGCGCTG 486

Db 316 C C C G C C G C C G G G C T G T C C G C G G C C C C A G T G C C C A C C G C C C C T G C C G C C G G C G C G C C C C T G 375

QY 487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546

Db 376 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 435

| Qy | 547      | CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC       | 597  |
|----|----------|--|------|
| Db | 436      | CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC    | 495  |
| Qy | 598      | GCGCCATCCCTGCCGCCCCGCTGCCGCAGTCTTCCCTCCAAGTCCCAGAGGACGACGAG    | 657  |
| Db | 496      | GCGCCATCCCCGCTGTCTGTCTGCCGCAGTCTCGCCCTCCAAGTCCCTGAGGACGACGAG   | 555  |
| Qy | 658      | CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----    | 711  |
| Db | 556      | CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG   | 615  |
| Qy | 712      | -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC                   | 750  |
| Db | promo616 | 225XC CAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC         | 675  |
| Qy | 751      | AGGGGCTCC--GGCTCAGTGGATGAGACCCCTTTTGTCTCTCCTGCTGCATCTGAGCCT    | 807  |
| Db | 676      | AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTGTCTCTCCTGCTGCATCTGAGCCT   | 735  |
| Qy | 808      | GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACTGTT      | 867  |
| Db | 736      | GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACTATT      | 792  |
| Qy | 868      | TCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGAAGTCTGCTGCTCTCTTCTTCT        | 927  |
| Db | 793      | TCGGCTGGTCAAGAGGATTTCCCATCTGTCTTGAAGTCTGCTGCTCTCTTCTTCT        | 852  |
| Qy | 928      | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA   | 987  |
| Db | 853      | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAACTTGTCAACA   | 912  |
| Qy | 988      | GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA    | 1047 |
| Db | 913      | GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA  | 972  |
| Qy | 1048     | GAGAGGGCAACAAATCCATTTCTAAATAGAGATTTTACAGCAATTTTACAGAAATTAGAAAT | 1107 |
| Db | 973      | GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAAAT   | 1032 |
| Qy | 1108     | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA   | 1167 |
| Db | 1033     | TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA   | 1092 |
| Qy | 1168     | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA--GACAAAGAGGATTTAGTTTGTAGT    | 1224 |
| Db | 1093     | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT   | 1152 |
| Qy | 1225     | GCAGCCCTTACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC              | 1269 |
| Db | 1153     | AACATCCTTACATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT  | 1212 |
| Qy | 1270     | AGAGTTGTGTCTCCAGAAAAGACAAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA  | 1329 |
| Db | 1213     | GAAGTTGTGTCTTCCAGAAAAGCAAAAGACAGTTTAAATGAAAGAGAGTTGCAGTGGAA    | 1272 |



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|----|------|---|------|
| Qy | 1330 | GCACCTGTGAGGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA | 1389 |
| Db | 1273 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAAACCATTTGAGCGAGTATGGGAAGTGAAA | 1332 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG         | 1437 |
| Db | 1333 | GATA--GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG   | 1389 |
| Qy | 1438 | GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG | 1497 |
| Db | 1390 | GAAAGTAAAGTGGATAAAAAATGTTTTCAGATAGCCTTGAGCAAATAATCACGAAAAA    | 1449 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCCAGAACCCTGTGAAGGAC  | 1557 |
| Db |      | TGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGCTTATAAGCAT        | 1509 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA  | 1614 |
| Db | 1510 | CGTTCAGGAGCATATATCATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA     | 1569 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA  | 1674 |
| Db | 1570 | ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA  | 1629 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT  | 1731 |
| Db | 1630 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC   | 1689 |
| Qy | 1732 | CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA  | 1791 |
| Db | 1690 | CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTAACA    | 1749 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG  | 1851 |
| Db | 1750 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG  | 1809 |
| Qy | 1852 | GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA  | 1911 |
| Db | 1810 | GAAGCATGTGAAAGTGAAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA | 1869 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT   | 1971 |
| Db | 1870 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT  | 1929 |
| Qy | 1972 | TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTCCTGATATTGTTATG   | 2031 |
| Db | 1930 | TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTCCTGACATTGTTATG    | 1989 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA   | 2091 |
| Db | 1990 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA   | 2049 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC  | 2151 |
| Db | 2050 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC  | 2106 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA  | 2208 |

|    |      |  |      |
|----|------|--|------|
| Db | 2107 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA        | 2166 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA       | 2268 |
| Db | 2167 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA       | 2226 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC      | 2328 |
| Db | 2227 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC      | 2286 |
| Qy | 2329 | TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG      | 2388 |
| Db | 2287 | TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCAITCTGAGCTAGTT      | 2346 |
| Qy | 238  |  |      |
| Db | 2347 | GAAGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATACATGAE      | 2406 |
| Qy | 2449 | GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A       | 2502 |
| Db | 2407 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA       | 2466 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCACAGCACAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA       | 2562 |
| Db | 2467 | TTTGAGTCAATGATAGAAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA       | 2526 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTTAGCCCAATTTACATAGTACAAAAGATGC---TGCA       | 2619 |
| Db | 2527 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAA5AGATACCCTGTTA       | 2586 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAGTTT       | 2679 |
| Db | 2587 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC      | 2646 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA       | 2739 |
| Db | 2647 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA       | 2706 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC       | 2799 |
| Db | 2707 | ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC      | 2766 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC       | 2856 |
| Db | 2767 | AGTTCTA <del>AACTGATb</del> CTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC | 2826 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG       | 2916 |
| Db | 2827 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATGCCTTGACACAGAATTG       | 2886 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA        | 2970 |
| Db | 2887 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA       | 2946 |
| Qy | 2971 | GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC       | 3030 |

Db 2947 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 3006  
 Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090  
 ||||| |||| |||| || ||||| ||||| ||||| |||||  
 Db 3007 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 3066  
 Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA 3150  
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||  
 Db 3067 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3126  
 Qy 3151 TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3127 TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3186  
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC 3270  
 ||||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||  
 Db 3187 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTTCAGC 3246  
 Qy 3271 ATTGTGAGTGAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330  
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3247 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3306  
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3307 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3366  
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT 3450  
 ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3367 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCT 3426  
 Qy 3451 CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTC050XA GTATTGGA 3510  
 ||||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||  
 Db 3427 CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3486  
 Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3487 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3546  
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCTGTATTATTTAT 3630  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3547 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTTCAGTGTTCTGTATTATTTAT 3606  
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAAACAAGAGTGTTAAGGAT 3690  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3607 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAAATAAGAATGTTAAGAT 3666  
 Qy 3691 GCCATGGCCAAAATC AAATCCCTGGATTGAAGCGCAAAGCAGA 37AAC 477  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3667 GCTATGGCTAAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAAGCTGA 3716

RESULT 5  
 US-09-789-386-1  
 ; Sequence 1, Application US/09789386  
 ; Patent No. US20020010324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MICHALOVICH, DAVID



|    |      |  |      |
|----|------|--|------|
| Db | 475  | TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC     | 534  |
| Qy | 751  | AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT    | 807  |
| Db | 535  | AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT    | 594  |
| Qy | 808  | GTGATACCTCCTCTGTCAGAAAAATTATGGATTGATGGAGCAGCCAGGTAACACTGTT     | 867  |
| Db | 595  | GTGATACGTCCTCTGTCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT   | 651  |
| Qy | 868  | TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT   | 927  |
| Db | 652  | TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT   | 711  |
| Qy | 928  | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA   | 987  |
| Db | 712  | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAACTTGTCAACA   | 771  |
| Qy | 988  | GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA    | 1047 |
| Db | 772  | GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA   | 831  |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAAATTAGAATAT  | 1107 |
| Db | 832  | GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC  | 891  |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA   | 1167 |
| Db | 892  | TCAGAAATGGGATCATCGTTTCAAGGCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA   | 951  |
| Qy | 1168 | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTA      CT    | 1224 |
| Db | 952  | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT   | 1011 |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC             | 1269 |
| Db | 1012 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT   | 1071 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA   | 1329 |
| Db | 1072 | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA     | 1131 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA   | 1389 |
| Db | 1132 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA   | 1191 |
| Qy | 1390 | GATACCTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG          | 1437 |
| Db | 1192 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTG    | 1248 |
| Qy | 1438 | GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG    | 1497 |
| Db | 1249 | GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACCTAACCGAAAAA     | 1308 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC    | 1557 |
| Db | 1309 | GATAGTGAGAGTAGTAATGATGATACCTTCTTTCCCCAGTACGCCAGAAAGGTATAAAGGAT | 1366 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA   | 1614 |
|    |      |  |      |
| Db | 1369 | CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA   | 1428 |
| Qy | 1615 | GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAAACAGATGAAAAAAAA | 1674 |
|    |      |  |      |
| Db | 1429 | ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA   | 1488 |
| Qy | 1675 | ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT   | 1731 |
|    |      |  |      |
| Db | 1489 | ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC   | 1548 |
| Qy | 1732 | CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA    | 1791 |
|    |      |  |      |
| Db | 9    | CCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAA↑↑↑↑AACA   | 1608 |
| Qy | 1792 | AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG   | 1851 |
|    |      |  |      |
| Db | 1609 | AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG   | 1668 |
| Qy | 1852 | GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA   | 1911 |
|    |      |  |      |
| Db | 1669 | GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA   | 1728 |
| Qy | 1912 | GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCCACAGCACAGCTT  | 1971 |
|    |      |  |      |
| Db | 1729 | ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT   | 1788 |
| Qy | 1972 | TGCCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG  | 2031 |
|    |      |  |      |
| Db | 1789 | TGCCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG  | 1848 |
| Qy | 2032 | GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA   | 2091 |
|    |      |  |      |
| Db | 1849 | GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA   | 1908 |
| Qy | 2092 | TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAAC  | 2151 |
|    |      |  |      |
| Db | 1909 | TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAAC  | 1965 |
| Qy | 2152 | CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA   | 2208 |
|    |      |  |      |
| Db | 1966 | CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA   | 2025 |
| Qy | 2209 | GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA   | 2268 |
|    |      |  |      |
| Db | 2026 | GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA   | 2085 |
| Qy | 2269 | TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTC    | 2328 |
|    |      |  |      |
| Db | 2086 | TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTC    | 2145 |
| Qy | 2329 | TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG   | 2388 |
|    |      |  |      |
| Db | 2146 | TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATCTGAGCTAGTT    | 2205 |

|    |       |   |      |
|----|-------|---|------|
| Qy | 2389  | GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA | 2448 |
| Db | 2206  | GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC   | 2265 |
| Qy | 2449  | GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A      | 2502 |
| Db | 2266  | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA    | 2325 |
| Qy | 2503  | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA    | 2562 |
| Db | 2326  | TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAACTCAGTGCTTTGCCACCTGAGGGA   | 2385 |
| Qy | 2563  | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA    | 2619 |
| Db | 23p59 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAAACACAAAAGATACCCTGTTA   | 2445 |
| Qy | 2620  | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT   | 2679 |
| Db | 2446  | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC   | 2505 |
| Qy | 2680  | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA    | 2739 |
| Db | 2506  | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA    | 2565 |
| Qy | 2740  | AGTGAAACATTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC     | 2799 |
| Db | 2566  | ACTGAAACGTTTCAGATTCTCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC      | 2625 |
| Qy | 2800  | AGTGCTAAAGATGATTC--TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC     | 2856 |
| Db | 2626  | AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC    | 2685 |
| Qy | 2857  | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTG   | 2916 |
| Db | 2686  | CACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCAATTGCCTTGACAGAATTG     | 2745 |
| Qy | 2917  | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA     | 2970 |
| Db | 2746  | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA    | 2805 |
| Qy | 2971  | GATGAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC   | 3030 |
| Db | 2806  | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT    | 2865 |
| Qy | 3031  | TCTGCTTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA   | 3090 |
| Db | 2866  | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTGTGAAA     | 2925 |
| Qy | 3091  | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGTA      | 3150 |
| Db | 2926  | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCCCATCTGCTATA     | 2985 |
| Qy | 3151  | TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG    | 3210 |
| Db | 2986  | TTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG   | 3045 |
| Qy | 3211  | AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC  | 3270 |

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Db      3046  |||||||||||||||||||||||||||||||||||||||||||||||||||| 3105
           AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTCATTGACAGTATTTCAGC
Qy      3271  ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
           ||||| || ||||||||||||||||||||||||||||||||||||
Db      3106  ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165
           ||||| ||||| ||||||||||||||||||||||||||||||||||||
Qy      3331  ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390
           ||||| ||||| ||||||||||||||||||||||||||||||||||||
Db      3166  ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3225
           ||||| ||||| ||||||||||||||||||||||||||||||||||||
Qy      3391  TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
           ||| | |||||||||||||||||||||||||||| ||||||||||||
Db      3226  TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285
           ||| | |||||||||||||||||||||||||||| ||||||||||||
Qy      3451  CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
           |||||||||||||||| |||| |||| |||| |||| || ||||||||||||
Db      3286  CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345
           |||||||||||||||| |||| |||| |||| |||| || ||||||||||||
Qy      3511  GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
           |||||||||||||||| |||||||||||||||| |||| |||| |||| ||||
Db      3346  GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405
           |||||||||||||||| |||||||||||||||| |||| |||| |||| ||||
Qy      3571  AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
           |||||||||||||||| |||||||||||||||| |||| |||| |||| ||||
Db      3406  AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465
           |||||||||||||||| |||||||||||||||| |||| |||| |||| ||||
Qy      3631  GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
           |||||||||||||||| |||||||||||||||| ||||||||||||||||
Db      3466  GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525
           |||||||||||||||| |||||||||||||||| ||||||||||||||||
Qy      3691  GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
           || ||||| ||||||||||||||||||||||||||||||||||||
Db      3526  GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575
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RESULT 6

US-09-893-348-22

; Sequence 22, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21



; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3579)  
; OTHER INFORMATION:  
US-09-893-348-22

Query Match 61.2%; Score 2289.2; DB 9; Length 3579;  
Best Local Similarity 81.5%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
          ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAG 432
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy      433 CCGCAGCCGGGCTGTCCGCGAGCTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      175 CCGCGCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCGCGCGGCGCGCCCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCC 546
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      235 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          || || || || || || || || || || || || || || || || || || || ||
Db      295 CCGGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354

Qy      598 GCGCCATCCCTGCCGCCGCTGCCGCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      355 GCGCCATCCCCGCTGTCTGTGCGCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      415 CCTCCGGCCCCGCGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy      712 -----CCCCCGCGCCCCCTTCCACGCGCGCCGCGCCCAAGCGC 750
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCGCGCCCAAGCGC 534

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTCTTCCTGCTGCATCTGAGCCT 807
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTCTTCCTGCTGCATCTGAGCCT 594
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|    |      |  |      |
|----|------|--|------|
| Qy | 808  | GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT    | 867  |
|    |      |  |      |
| Db | 595  | GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT    | 651  |
| Qy | 868  | TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT   | 927  |
|    |      |  |      |
| Db | 652  | TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT   | 711  |
| Qy | 928  | CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA   | 987  |
|    |      |  |      |
| Db | 712  | CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAAATTTGTCAACA  | 771  |
| Qy | 988  | GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA    | 1047 |
|    |      |  |      |
| Db | 772  | GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA   | 831  |
| Qy | 1048 | GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT   | 1107 |
|    |      |  |      |
| Db | 832  | GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC | 891  |
| Qy | 1108 | TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA   | 1167 |
|    |      |  |      |
| Db | 892  | TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA  | 951  |
| Qy | 1168 | AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT   | 1224 |
|    |      |  |      |
| Db | 952  | AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT   | 1011 |
| Qy | 1225 | GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC             | 1269 |
|    |      |  |      |
| Db | 1012 | AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTTGGTTAAAGAGGAT  | 1071 |
| Qy | 1270 | AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA   | 1329 |
|    |      |  |      |
| Db | 1072 | GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA     | 1131 |
| Qy | 1330 | GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA   | 1389 |
|    |      |  |      |
| Db | 1132 | GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA   | 1191 |
| Qy | 1390 | GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG          | 1437 |
|    |      |  |      |
| Db | 1192 | GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG   | 1248 |
| Qy | 1438 | GAAAGTAAAGTGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG     | 1497 |
|    |      |  |      |
| Db | 1249 | GAAAGTAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA     | 1308 |
| Qy | 1498 | GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC    | 1557 |
|    |      |  |      |
| Db | 1309 | GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT   | 1368 |
| Qy | 1558 | AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA   | 1614 |
|    |      |  |      |
| Db | 1369 | CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA    | 1428 |

|    |      |                  |                        |                     |                  |       |      |
|----|------|------------------|------------------------|---------------------|------------------|-------|------|
| Qy | 1615 | GCAAACAC         | TTTCCCTTTGTTAGAA       | GATCATACTTCAGAAA    | ATAAAACAGATGAAAA | AAAAA | 1674 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1429 | ACAAACAT         | TTTTCCCTTTGTTAGG       | AGATCCTACTTCAGAAA   | ATAAGACCGATGAAAA | AAAAA | 1488 |
| Qy | 1675 | ATAGAAGAAAGGAAGG | CCCAAATTATAACAGAG      | AAG--ACTAGCCCCAAA   | ACGTCAAAT        |       | 1731 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1489 | ATAGAAGAAAAGAAGG | CCCAAATAGTAACAGAG      | AGAATACTAGCACCAA    | AAACATCAAAC      |       | 1548 |
| Qy | 1732 | CCTTTCCCTTG      | TAGCAGTACAGGATTCTGAGG  | CAGATTATGTTACAAC    | CAGATACCTTATCA   |       | 1791 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1549 | CCTTTTCTTG       | TAGCAGCACAGGATTCTGAGAC | CAGATTATGTCACAAC    | CAGATAATTTAACA   |       | 1608 |
| Qy | 1792 | AAGGTGACTGAGGC   | CAGCAGTGTCAAACATGCCTG  | AAGGTCTGACGCCAGATT  | TTAGTTCAG        |       | 1851 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1609 | AAGGTGACTGAGGA   | AGTCGTGGCAAACATGCCTG   | AAGGCCCTGACTCCAGATT | TTAGTACAG        |       | 1668 |
| Qy | 1852 | GAAGCATGTGAAAGT  | GAACTGAATGAAGCCACAGG   | TACAAAGATTGCTTATG   | AAACAAAA         |       | 1911 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1669 | GAAGCATGTGAAAGT  | GAAATTGAATGAAGTTACTGG  | TACAAAGATTGCTTATG   | AAACAAAA         |       | 1728 |
| Qy | 1912 | GTGGACTTGGTCCAA  | ACATCAGAAGCTATACAAGA   | ATCACTTTACCCACAGC   | ACAGCTT          |       | 1971 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1729 | ATGGACTTGGTTCAA  | ACATCAGAAGTTATGCAAGAG  | TCACTCTATCCTGCAGC   | ACAGCTT          |       | 1788 |
| Qy | 1972 | TGCCCCATCATTTG   | AGGAAGCTGAAGCAACTCCGT  | CACCAGTTTTGCCTGAT   | TATGTTATG        |       | 2031 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1789 | TGCCCCATCATTTG   | AAGAGTCAGAAGCTACTCCTT  | CACCAGTTTTGCCTGAC   | ATTGTTATG        |       | 1848 |
| Qy | 2032 | GAAGCACCATTAAAT  | TCTCTCCTTCCAAGCGCTGGT  | GTCTCTGTAGTGCAGCC   | CAGTGTA          |       | 2091 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1849 | GAAGCACCATTGAAT  | TCTGCAGTTCCTAGTGTCTGGT | GTCTCCGTGATACAGCC   | CAGTCA           |       | 1908 |
| Qy | 2092 | TCCCCACTGGAAGC   | ACCTCCTCCAGTTAGTTATG   | ACAGTATAAAGCTTGAGC  | CTGAAAAAC        |       | 2151 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1909 | TCACCATTAGAAG--  | CTTCTTCAGTTAATTATGAA   | AGCATAAACATGAGCCT   | GAAAAAC          |       | 1965 |
| Qy | 2152 | CCCCCACCATATGA   | AGAAGCCATGAATGTAGCA    | CT--AAAAGCTTTGGGA   | ACAAAGGAA        |       | 2208 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 1966 | CCCCCACCATATGA   | AGAGGCCATGAGTGTATCA    | CTAAAAAAGTATCAGGA   | ATAAAGGAA        |       | 2025 |
| Qy | 2209 | GGAATAAAAGAGCCT  | GAAAGTTTTTAATGCAGCT    | GTTCAGGAAACAGAAGCT  | CTCTATATA        |       | 2268 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 2026 | GAAATTAAAGAGCCT  | GAAAAATATTAATGCAGCT    | CTTCAAGAAACAGAAGCT  | CTCTATATA        |       | 2085 |
| Qy | 2269 | TCCATTGCGTGTGAT  | TTAATTAAGAAACAAAGCT    | CTCCACTGAGCCAAGTCC  | CAGATTTT         |       | 2328 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 2086 | TCTATTGCATGTGAT  | TTAATTAAGAAACAAAGCT    | TTTCTGCTGAACCAGCT   | CCGGATTT         |       | 2145 |
| Qy | 2329 | TCTAATTATT       | CAGAAATAGCAAAATTCGAG   | AAGTCGGTGCCCGAACAC  | GCTGAGCTAGTG     |       | 2388 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 2146 | TCTGATTATT       | CAGAAATGGCAAAAGTTGA    | CAGCCAGTGCCTGATCAT  | TCTGAGCTAGTT     |       | 2205 |
| Qy | 2389 | GAGGATTCCTCACCT  | GAACTCTGAACCAGTTGACT   | TATTTAGTGATGATT     | CGATTCCTGAA      |       | 2448 |
|    |      |                  |                        |                     |                  |       |      |
| Db | 2206 | GAAGATTCCTCACCT  | GATTCTGAACCAGTTGACT    | TATTTAGTGATGATT     | CAATACCTGAC      |       | 2265 |
| Qy | 2449 | GTCCCACAAACACA   | AAGAGGAGGCTGTGATGCT    | CATGAAGGAGAGTCTCA   | CTGA-----A       |       | 2502 |

|    |      |   |      |
|----|------|---|------|
| Db | 2266 | GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA  | 2325 |
| Qy | 2503 | GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA  | 2562 |
| Db | 2326 | TTTGAGTCAATGATAGAAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA | 2385 |
| Qy | 2563 | GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA  | 2619 |
| Db | 2386 | GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA  | 2445 |
| Qy | 2620 | TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT | 2679 |
| Db | 2446 | CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC | 2505 |
| Qy | 2680 | AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA  | 2739 |
| Db | 2506 | AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA  | 2565 |
| Qy | 2740 | AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC  | 2799 |
| Db | 2566 | ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC | 2625 |
| Qy | 2800 | AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC  | 2856 |
| Db | 2626 | AGTTCTAAAAC TGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC | 2685 |
| Qy | 2857 | GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG | 2916 |
| Db | 2686 | CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAATTG   | 2745 |
| Qy | 2917 | CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA   | 2970 |
| Db | 2746 | CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA  | 2805 |
| Qy | 2971 | GATGAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTC   | 3030 |
| Db | 2806 | GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT  | 2865 |
| Qy | 3031 | TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA | 3090 |
| Db | 2866 | TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA  | 2925 |
| Qy | 3091 | GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA  | 3150 |
| Db | 2926 | GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA  | 2985 |
| Qy | 3151 | TTGTGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG  | 3210 |
| Db | 2986 | TTTTGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG  | 3045 |
| Qy | 3211 | AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC | 3270 |
| Db | 3046 | AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC | 3105 |
| Qy | 3271 | ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG | 3330 |



Query Match 29.1%; Score 1088.8; DB 13; Length 1980;  
Best Local Similarity 83.5%; Pred. No. 1.3e-269;  
Matches 1289; Conservative 0; Mismatches 237; Indels 18; Gaps 4;

|    |      |  |      |
|----|------|--|------|
| Qy | 2215 | AAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCTCATT | 2274 |
|    |      |  |      |
| Db | 28   | AAAGAGCCTGAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT    | 87   |
| Qy | 2275 | GCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAAT   | 2334 |
|    |      |  |      |
| Db | 88   | GCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGATTTCTCTGAT    | 147  |
| Qy | 2335 | TATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGAT   | 2394 |
|    |      |  |      |
| Db | 148  | TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTTGAAGAT   | 207  |
| Qy | 2395 | TCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCA  | 2454 |
|    |      |  |      |
| Db | 208  | TCCTCACCTGATTCCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA  | 267  |
| Qy | 2455 | CAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----AGTGTCT    | 2508 |
|    |      |  |      |
| Db | 268  | CAAAAACAAGGTGAAACTGTGATGCTTG'TGAAAGAAAGTCTCACTGAGACTTCATTTGAG  | 327  |
| Qy | 2509 | GAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAG    | 2568 |
|    |      |  |      |
| Db | 328  | TCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAG   | 387  |
| Qy | 2569 | CCATATTTAGAGTCTTTTCAGCCCAATTACATAGTACAAAAGATGC---TGATCTAAT     | 2625 |
|    |      |  |      |
| Db | 388  | CCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGAT   | 447  |
| Qy | 2626 | GACATTTCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACT  | 2685 |
|    |      |  |      |
| Db | 448  | GAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTCAGTACT  | 507  |
| Qy | 2686 | GCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAA   | 2745 |
|    |      |  |      |
| Db | 508  | GCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAA   | 567  |
| Qy | 2746 | ACATTTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTGCT    | 2805 |
|    |      |  |      |
| Db | 568  | ACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTCCT  | 627  |
| Qy | 2806 | AAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA   | 2862 |
|    |      |  |      |
| Db | 628  | AAAAC'TGATTCATTTTCTAAATTAGCCAGGAATATACTGACCTAGAAGTATCCCACAAA   | 687  |
| Qy | 2863 | AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGT   | 2922 |
|    |      |  |      |
| Db | 688  | AGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATTGCCTTGACAGAATTGCCCAT    | 747  |
| Qy | 2923 | GACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCAGATGAA    | 2976 |
|    |      |  |      |
| Db | 748  | GACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGAC   | 807  |

|    |      |   |      |
|----|------|---|------|
| Qy | 2977 | TTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCT   | 3036 |
|    |      |   |      |
| Db | 808  | TTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCT    | 867  |
| Qy | 3037 | TTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCA    | 3096 |
|    |      |   |      |
| Db | 868  | TTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTC'TTGTGAAAGAAGCT   | 927  |
| Qy | 3097 | GAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGCTGATTGTCA    | 3156 |
|    |      |   |      |
| Db | 928  | GAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCA    | 987  |
| Qy | 3157 | GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACT    | 3216 |
|    |      |   |      |
| Db | 988  | GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACT    | 1047 |
| Qy | 3217 | GGAGTGGTGT'TTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTC    | 3276 |
|    |      |   |      |
| Db | 1048 | GGAGTGGTGT'TTGGTGCCAGCCTATTCCAGCTGCTTTTCATTGACAGTATTTCAGCATTGTG | 1107 |
| Qy | 3277 | AGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATAT    | 3336 |
|    |      |   |      |
| Db | 1108 | AGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC    | 1167 |
| Qy | 3337 | AAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATATTTA   | 3396 |
|    |      |   |      |
| Db | 1168 | AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATATCTG   | 1227 |
| Qy | 3397 | GAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAAGAAATACAGTAATTCTGCTCTTGGT  | 3456 |
|    |      |   |      |
| Db | 1228 | GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTAAGTACAGTAATTCTGCTCTTGGT | 1287 |
| Qy | 3457 | CATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT   | 3516 |
|    |      |   |      |
| Db | 1288 | CATGTGAACAGCACGATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT    | 1347 |
| Qy | 3517 | TCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGT     | 3576 |
|    |      |   |      |
| Db | 1348 | TCTCTGGAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGT    | 1407 |
| Qy | 3577 | CTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGG    | 3636 |
|    |      |   |      |
| Db | 1408 | CTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGG    | 1467 |
| Qy | 3637 | CATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATG    | 3696 |
|    |      |   |      |
| Db | 1468 | CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG    | 1527 |
| Qy | 3697 | GCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA                    | 3740 |
|    |      |   |      |
| Db | 1528 | GCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA                    | 1571 |

```

; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 165
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-165

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Query Match          21.6%; Score 809.8; DB 13; Length 2782;
Best Local Similarity 99.8%; Pred. No. 1.7e-197;
Matches 811; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      14 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 73
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Db      462 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 521

Qy      74 CAGAAGCAGTCTCATTTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG 133
      |||
Db      522 GAGAAGCAGTCTCATTTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG 581

Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
      |||
Db      582 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 641

Qy      194 CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 253
      |||
Db      642 CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 701

Qy      254 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC 313
      |||
Db      702 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC 761

Qy      314 CGCCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG 373
      |||
Db      762 CGCCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG 821

Qy      374 AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC 433
      |||
Db      822 AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC 881

Qy      434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCCGCCCGCGCCGCTGCTGGACT 493
      |||

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Db      882 CCGCAGCCGGGCTGTCCGCACTGCGGTGCCGCCCCGCCGCCGCCGCCGCTGCTGGACT 941
Qy      494 TCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553
      |||
Db      942 TCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 1001
      |||
Qy      554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613
      |||
Db      1002 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 1061
      |||
Qy      614 CCGCTGCCGCACTCCTGCCCTCCAAGCTCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673
      |||
Db      1062 CCGCTGCCGCACTCCTGCCCTCCAAGCTCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 1121
      |||
Qy      674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733
      |||
Db      1122 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 1181
      |||
Qy      734 CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTGTCTCTCCTG 793
      |||
Db      1182 CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTGTCTCTCCTG 1241
      |||
Qy      794 CTGCATCTGAGCCTGTGATACCCTCCTCTGCAG 826
      |||
Db      1242 CTGCATCTGAACCTGTGATACCCTCCTCTGCAG 1274

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# RESULT 9

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US-09-789-386-5
; Sequence 5, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-5

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Query Match          13.3%; Score 497.4; DB 9; Length 1122;
Best Local Similarity 92.7%; Pred. No. 3.4e-117;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237

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|    |      |  |      |
|----|------|--|------|
| Db | 556  | <br>GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC  | 615  |
| Qy | 3238 | TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACATTGCC     | 3297 |
| Db | 616  | <br>CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC | 675  |
| Qy | 3298 | TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC       | 3357 |
| Db | 676  | <br>TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC   | 735  |
| Qy | 3358 | CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA      | 3417 |
| Db | 736  | <br>CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT  | 795  |
| Qy | 3418 | GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA       | 3477 |
| Db | 796  | <br>GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG   | 855  |
| Qy | 3478 | GAAGTGAAGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG       | 3537 |
| Db | 856  | <br>GAAGTGAAGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG   | 915  |
| Qy | 3538 | ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT       | 3597 |
| Db | 916  | <br>ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT  | 975  |
| Qy | 3598 | CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT       | 3657 |
| Db | 976  | <br>CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT   | 1035 |
| Qy | 3658 | TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC       | 3717 |
| Db | 1036 | <br>TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC   | 1095 |
| Qy | 3718 | CCTGGATTGAAGCGCAAAGCAGA  | 3740 |
| Db | 1096 | <br>CCTGGATTGAAGCGCAAAGCTGA  | 1118 |

RESULT 10

US-10-175-523-156

; Sequence 156, Application US/10175523

; Publication No. US20030096264A1

; GENERAL INFORMATION:

; APPLICANT: Brockman, Jeffrey

; APPLICANT: Evans, David

; APPLICANT: Hook, Derek

; APPLICANT: Klimczak, Leszek

; APPLICANT: Laeng, Pascal

; APPLICANT: Palfreyman, Michael

; APPLICANT: Rajan, Prithi

; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)

; FILE REFERENCE: 3235/1J795-US3

; CURRENT APPLICATION NUMBER: US/10/175,523

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: US 60/299,151

```

; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-156

```

```

Query Match          13.3%; Score 497.4; DB 15; Length 1160;
Best Local Similarity 92.7%; Pred. No. 3.5e-117;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```

```

Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
          |||
Db      228 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 287
          |||

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAAACGGCCTACATTGCC 3297
          |||
Db      288 CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 347
          |||

Qy      3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
          |||
Db      348 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 407
          |||

Qy      3358 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
          |||
Db      408 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 467
          |||

Qy      3418 GAGGAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTTCATGTGAACAGCACAATAAAA 3477
          |||
Db      468 GAGGAGTTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTTCATGTGAACAGCACAATAAA 527
          |||

Qy      3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
          |||
Db      528 GAACTCAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 587
          |||

Qy      3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
          |||
Db      588 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 647
          |||

Qy      3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
          |||
Db      648 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 707
          |||

Qy      3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
          |||

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Db          708 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 767
Qy          3718 CCTGGATTGAAGCGCAAAGCAGA 3740
              |||
Db          768 CCTGGATTGAAGCGCAAAGCTGA 790

```

RESULT 11

US-10-439-388-62

```

; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens

```

US-10-439-388-62

```

Query Match          13.3%; Score 497.4; DB 12; Length 1785;
Best Local Similarity 92.7%; Pred. No. 4.8e-117;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```

```

Qy          3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
              |||
Db          247 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 306

Qy          3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297
              |||
Db          307 CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 366

Qy          3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
              |||
Db          367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 426

Qy          3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
              |||
Db          427 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 486

Qy          3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAA 3477
              |||
Db          487 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 546

Qy          3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
              |||
Db          547 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 606

Qy          3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTC AATGGTCTGACACTACTGATTTTAGCT 3597

```



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      |||
Db      877 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGAAGTTGCTATATCT 936
      |||
Qy      3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAA 3477
      |||
Db      937 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 996
      |||
Qy      3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAAGTGTG 3537
      |||
Db      997 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG 1056
      |||
Qy      3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
      |||
Db      1057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 1116
      |||
Qy      3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
      |||
Db      1117 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176
      |||
Qy      3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
      |||
Db      1177 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1236
      |||
Qy      3718 CCTGGATTGAAGCGCAAAGCAGA 3740
      |||
Db      1237 CCTGGATTGAAGCGCAAAGCTGA 1259

```

# RESULT 13

US-09-765-205-5

; Sequence 5, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 1610

; TYPE: DNA

; ORGANISM: human

US-09-765-205-5

Query Match 13.3%; Score 495.8; DB 9; Length 1610;

Best Local Similarity 92.5%; Pred. No. 1.2e-116;

Matches 521; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

```

Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
      |||
Db      687 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 746
      |||
Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCTGAGTGTGTAACGGCCTACATTGCC 3297

```

|    |      |   |      |
|----|------|---|------|
| Db | 747  | CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTGCC | 806  |
| Qy | 3298 | TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC    | 3357 |
| Db | 807  | TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC    | 866  |
| Qy | 3358 | CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA   | 3417 |
| Db | 867  | CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT   | 926  |
| Qy | 3418 | GAGGAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAA  | 3477 |
| Db | 927  | GAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTCAACTGCACGATAAAG   | 986  |
| Qy | 3478 | GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG    | 3537 |
| Db | 987  | GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG    | 1046 |
| Qy | 3538 | ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCT     | 3597 |
| Db | 1047 | ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT    | 1106 |
| Qy | 3598 | CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT    | 3657 |
| Db | 1107 | CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT    | 1166 |
| Qy | 3658 | TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC    | 3717 |
| Db | 1167 | TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC    | 1226 |
| Qy | 3718 | CCTGGATTGAAGCGCAAAGCAGA   | 3740 |
| Db | 1227 | CCTGGATTGAAGCGCAAAGCTGA   | 1249 |

RESULT 14

US-09-789-386-3

; Sequence 3, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30165-C1

; CURRENT APPLICATION NUMBER: US/09/789,386

; CURRENT FILING DATE: 2001-02-21

; PRIOR APPLICATION NUMBER: U.K. 9916898.1

; PRIOR FILING DATE: 1999-07-19

; PRIOR APPLICATION NUMBER: U.K. 9816024.5

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: US 09/359,208

; PRIOR FILING DATE: 1999-07-22

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 868

; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (91)(413)  
US-09-789-386-3

Query Match 12.9%; Score 483.6; DB 9; Length 868;  
Best Local Similarity 76.8%; Pred. No. 1e-113;  
Matches 668; Conservative 0; Mismatches 166; Indels 36; Gaps 5;

```
Qy      830 AAATTATGGATTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTC 889
      ||| ||||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2 AAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTTCGGCTGGTCAAGAGGATTTC 61

Qy      890 CATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCTTCTCTATCTCCTCTCTCAACTGTTT 949
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      62 CATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCTTCTCTGTCTCCTCTCTCAGCCGCTT 121

Qy      950 CTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCAGTGTATCCTCAGAAGGAACAA 1009
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      122 CTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCCACTGAAGGAACAC 181

Qy      1010 TTGAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTG 1069
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      182 TTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCAAAAACCTTACTCA 241

Qy      1070 TAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTA 1129
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      242 TAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATGGGATCATCGTTCA 301

Qy      1130 AAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTG 1189
      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      302 GTGTCTCTCCAAAAGCAGAACTGCGCGTAATAGTAGCAAATCCTAGGGAAGAAATAATCG 361

Qy      1190 TGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAG 1246
      ||| | |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      362 TGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAATAACATCCTTCATANTCAACAAG 421

Qy      1247 AATCACCT-----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGA 1291
      | | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      422 AGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTGTCTTCAGAAAAAG 481

Qy      1292 CAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATG 1351
      ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      482 CAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATGAGGGAGGAATATG 541

Qy      1352 CAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGG 1411
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      542 CAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATA---GTAAGGAAGATAGTG 598

Qy      1412 ATGTGCTGGCTGCTAGAGCT-----AATGTGGAAGTAAAGTGGACAGAAAAAT 1459
      || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      599 ATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTGGAAAGTAAAGTGGATAAAAAAT 658

Qy      1460 GCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGATAGTGAAGGCAGAAATGAGG 1519
      | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db          659  GTTTTGCAGATAGCCTTGAGCAAAC TAATCACGAAAAAGATAGTGAGAGTAGTAATGATG 718
Qy          1520 ATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGACAGCTCCAGAGCATATATTACCT 1579
           || ||||| ||||| ||||| | | ||||| | || ||||| ||||| || |
Db          719  ATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTTCAGGAGCATATATCACAT 778
Qy          1580 GTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCAAGCAAAACACTTTCCCTTTGTTAG 1636
           ||||| ||||| | ||||| || |||| | || ||||| || ||||| |||||
Db          779  GTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCAACAAACATTTTCCCTTTGTTAG 838
Qy          1637 AAGATCATACTTCAGAAAATAAAACAGATG 1666
           ||||| ||||| ||||| || |||||
Db          839  GAGATCCTACTTCAGAAAATAAGACCGATG 868

```

### RESULT 15

```

US-09-960-352-8477
; Sequence 8477, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH
LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8477
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8
US-09-960-352-8477

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Query Match 10.0%; Score 375.6; DB 10; Length 422;  
Best Local Similarity 93.1%; Pred. No. 4.3e-86;  
Matches 393; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

[illegible]

Qy 3522 GAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGAC 3581  
 ||||||||||||||||||||| ||||| |||||||||||||||||||||  
 Db 241 GAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGAC 300  
 Qy 3582 ACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCA 3641  
 ||||| ||||| ||||||||| ||||||||||||| ||||||||||||| |||||||||  
 Db 301 ACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCA 360  
 Qy 3642 GGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAA 3701  
 || ||| ||||||||||||| ||||||||||||| ||||| ||||||| ||||| |||  
 Db 361 GGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAA 420  
 Qy 3702 AA 3703  
 ||  
 Db 421 AA 422

Search completed: January 23, 2004, 15:24:40  
 Job time : 1133.66 secs